adl gene. Homo
Lung cancer associ

ALIGNMENTS

RESULT 1
AAQ46688
ID AAQ46688 standard; cDNA to mRNA; 1611 BP.
XX
AC AAQ46688;
XX
DT 23-DEC-1993 (first entry)
XX
DE Human pp60 c-src gene.
XX
KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX
OS Homo sapiens.
XX
PN WO9314193-A.
XX
PD 22-JUL-1993.
XX
PF 05-JAN-1993; 93WO-US000445.
XX
PR 06-JAN-1992; 92US-0820011.
XX
PA (UYYA) UNIV YALE.
XX
PI Bell L, Luthringer DJ, Madri JA, Warren SL;
XX
DR WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX
PT Genetically engineered endothelial cells - which exhibit enhanced
PT cell migration, urokinase-type plasminogen activator activity,
PT and reduced mononuclear cell adhesion and fibronectin prodn

XX
PS Disclosure; Page 69-72; 91pp; English.
XX
CC The DNA encoding a portion or (more preferably) the entire pp60
CC c-src polypeptide is used to transform endothelial cells.
CC Transformed cells produce increased amounts of pp60 c-src and have
CC improved therapeutic properties. They migrate at faster rates than
CC non-transformed counterparts; have an enhanced ability to inhibit
CC the formation of thrombi and/or dissolve thrombi once they have
CC formed and exhibit reduced mononuclear cell adhesion. They can also
CC be used to improve the success of surgical procedures such as
CC coronary angioplasty, heart bypass surgery, vessel graft and stent
CC implantation.
XX
SQ Sequence 1611 BP; 334 A; 507 C; 504 G; 266 T; 0 other;

[redacted]ery Match 99.9%; Score 1609.4; DB 14; Length 1611;
[redacted]st Local Similarity 99.9%; Pred. No. 2.9e-294;
Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    1561 gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag 1611
Db    1561 gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag 1611
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RESULT 2
AAS[redacted]

ALIGNMENTS

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US-07-820-011A-3
; Sequence 3, Application US/07820011A
; Patent No. 5336615
;  GENERAL INFORMATION:
;    APPLICANT:  Bell, Leonard
;    APPLICANT:  Madri, Joseph A.
;    APPLICANT:  Warren, Stephen L.
;    APPLICANT:  Luthringer, Daniel J.
;    TITLE OF INVENTION:  Genetically Engineered
;    TITLE OF INVENTION:  Endothelial Cells Exhibiting Enhanced
;    TITLE OF INVENTION:  Migration
;    TITLE OF INVENTION:  and Plasminogen Activator Activity
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairifield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb storage
;      COMPUTER:  IBM PC XT
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 2.10
;      SOFTWARE:  Displaywrite 3
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/820,011A
;      FILING DATE:  19920106
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  LB-101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255 1400
;      TELEFAX:  (203) 254 1101
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1611
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapien
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  Chromosome 20
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; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Tanaka, Akio
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: Human Cellular src Gene:
; TITLE: Nucleotide Sequence and Derived Amino
; TITLE: Acid Sequence of the Region Coding for
; TITLE: the Carboxy-Terminal Two-Thirds of
; TITLE: pp60c-src
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; ISSUE: 5
; PAGES: 1122-1129
; DATE: May, 1985
; PUBLICATION INFORMATION:
; AUTHORS: Tanaka, Akio
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Arthur, Richard R.
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: DNA Sequence Encoding the
; TITLE: Amino-Terminal Region of the Human c-src
; TITLE: Protein: Implications of Sequence
; TITLE: Divergence among src-Type Kinase
; TITLE: Oncogenes
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 7
; ISSUE: 5
; PAGES: 1978-1983
; DATE: May, 1987
US-07-820-011A-3

Query Match 99.9%; Score 1609.4; DB 1; Length 1611;
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Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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KW   Endothelial; tyrosine kinase protein; pp60 c-src; ss.
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PR   06-JAN-1992;   92US-0820011.
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PI   Bell L,  Luthringer DJ,  Madri JA,  Warren SL;
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DR   WPI; 1993-243209/30.
DR   P-PSDB; AAR39705.
XX
PT   Genetically engineered endothelial cells - which exhibit enhanced
PT   cell migration, urokinase-type plasminogen activator activity,
PT   and reduced mononuclear cell adhesion and fibronectin prodn
XX
PS   Disclosure; Page 75-77; 91pp; English.
XX
CC   The DNA encoding a portion or (more preferably) the entire pp60
CC   c-src polypeptide (Given in AAQ46688) is used to transform endothelial
CC   cells. Transformed cells produce increased amounts of pp60 c-src and
CC   have improved therapeutic properties. They migrate at faster rates
CC   than non-transformed counterparts; have an enhanced ability to
CC   inhibit the formation of thrombi and/or dissolve thrombi once they
CC   have formed and exhibit reduced mononuclear cell adhesion.  They can
CC   also be used to improve the success of surgical procedures such as
CC   coronary angioplasty, heart bypass surgery, vessel graft and stent
CC   implantation.
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SQ   Sequence   536 AA;


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;    APPLICANT:  Madri, Joseph A.
;    APPLICANT:  Warren, Stephen L.
;    APPLICANT:  Luthringer, Daniel J.
;    TITLE OF INVENTION:  Genetically Engineered
;    TITLE OF INVENTION:  Endothelial Cells Exhibiting Enhanced
;    TITLE OF INVENTION:  Migration
;    TITLE OF INVENTION:  and Plasminogen Activator Activity
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairifield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
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;      MEDIUM TYPE:  5.25 inch, 360 Kb storage
;      COMPUTER:  IBM PC XT
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 2.10
;      SOFTWARE:  Displaywrite 3
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/820,011A
;      FILING DATE:  19920106
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  LB-101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255 1400
;      TELEFAX:  (203) 254 1101
;  INFORMATION FOR SEQ ID NO:  4:
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;    MOLECULE TYPE:  Protein
;    HYPOTHETICAL:  No
;    FRAGMENT TYPE:  Complete Sequence
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapien
;    PUBLICATION INFORMATION:
;      AUTHORS:  Anderson, Stephen K.
;      AUTHORS:  Gibbs, Carol P.
;      AUTHORS:  Tanaka, Akio
;      AUTHORS:  Kung, Hsing-Jien
;      AUTHORS:  Fujita, Donald J.
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;      TITLE:  Nucleotide Sequence and Derived Amino
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;      JOURNAL:  Molecular and Cellular Biology
;      VOLUME:  5
;      ISSUE:  5
;      PAGES:  1122-1129
;      DATE:  May, 1985
;    PUBLICATION INFORMATION:
;      AUTHORS:  Tanaka, Akio
;      AUTHORS:  Gibbs, Carol P.
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; AUTHORS: Arthur, Richard R.
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: DNA Sequence Encoding the
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	35	314	19.5	3026	23	AAS92456	DNA encoding novel
	36	296.2	18.4	1548	20	AAV81743	Human SAD encoding
c	37	284	17.6	7607	14	AAQ49754	pTK gene LpTK-2.
c	38	284	17.6	7607	16	AAT03097	Protein tyrosine-k
	39	260	16.1	4515	23	ABL07083	Drosophila melanog
	40	259	16.1	3653	24	ABI99918	Rat mucocardial ce
	41	256	15.9	5520	18	AAT61865	c-abl gene. Homo
	42	252	15.6	271	19	AAV20446	Human c-srcl oncog
	43	249.6	15.5	3623	19	AAV20457	Human c-abl oncoge
	44	249.6	15.5	3780	18	AAT61864	c-abl gene. Homo
	45	239.8	14.9	1056	21	AAF18064	Lung cancer associ

ALIGNMENTS

RESULT 1
AAQ46688
ID AAQ46688 standard; cDNA to mRNA; 1611 BP.
XX
AC AAQ46688;
XX
DT 23-DEC-1993 (first entry)
XX
DE Human pp60 c-src gene.
XX
KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX
OS Homo sapiens.
XX
PN WO9314193-A.
XX
PD 22-JUL-1993.
XX
PF 05-JAN-1993; 93WO-US000445.
XX
PR 06-JAN-1992; 92US-0820011.
XX
PA (UYYA) UNIV YALE.
XX
PI Bell L, Luthringer DJ, Madri JA, Warren SL;
XX
DR WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX
PT Genetically engineered endothelial cells - which exhibit enhanced
PT cell migration, urokinase-type plasminogen activator activity,
PT and reduced mononuclear cell adhesion and fibronectin prodn

```
;       AUTHORS:  Arthur, Richard R.
;       AUTHORS:  Anderson, Stephen K.
;       AUTHORS:  Kung, Hsing-Jien
;       AUTHORS:  Fujita, Donald J.
;       TITLE:  DNA Sequence Encoding the
;       TITLE:  Amino-Terminal Region of the Human c-src
;       TITLE:  Protein: Implications of Sequence
;       TITLE:  Divergence among src-Type Kinase
;       TITLE:  Oncogenes
;       JOURNAL:  Molecular and Cellular Biology
;       VOLUME:  7
;       ISSUE:  5
;       PAGES:  1978-1983
;       DATE:  May, 1987
US-07-820-011A-4


alignment_scores:
            Quality: 2834.00              Length:    536
              Ratio:  5.287                Gaps:      0
 Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-444-711-1 x US-07-820-011A-4   ..

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      1 MetGlySerAsnLysSerLysProLysAspAlaSerGlnArgArgArgSe 17

     51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCG 100
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    101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACCGCGGCCCC 150
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     34 laSerGlnThrProSerLysProAlaSerAlaAspGlyHisArgGlyPro 50

    151 AGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTT 200
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    201 CAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCG 250
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     67 eAsnSerSerAspThrValThrSerProGlnArgAlaGlyProLeuAlaG 84

    251 GTGGAGTGACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAG 300
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     84 lyGlyValThrThrPheValAlaLeuTyrAspTyrGluSerArgThrGlu 100

    301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACAC 350
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    351 GGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCT 400
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    117 rGluGlyAspTrpTrpLeuAlaHisSerLeuSerThrGlyGlnThrGlyT 134

    401 ACATCCCCAGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAG 450
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    134 yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 150

    451 TGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAA 500
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    151 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeuLeuAs 167

    501 TGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGA 550
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    167 nAlaGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThrL 184

    551 AAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600
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    184 ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 200

    601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 650
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    651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
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    217 eThrSerArgThrGlnPheAsnSerLeuGlnGlnLeuValAlaTyrTyrS 234

    701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
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    234 erLysHisAlaAspGlyLeuCysHisArgLeuThrThrValCysProThr 250

    751 TCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCG 800
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    851 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900
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PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG23778.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 23769; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1699 BP; 364 A; 532 C; 511 G; 292 T; 0 other;

Query Match 78.8%; Score 1269; DB 23; Length 1699;
Best Local Similarity 95.0%; Pred. No. 3.7e-230;
Matches 1359; Conservative 0; Mismatches 5; Indels 67; Gaps 2;

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; Sequence 4, Application PC/TUS9300445
;  GENERAL INFORMATION:
;    APPLICANT:  Bell, Leonard
;    APPLICANT:  Madri, Joseph A.
;    APPLICANT:  Warren, Stephen L.
;    APPLICANT:  Luthringer, Daniel J.
;    TITLE OF INVENTION:  Genetically Engineered
;    TITLE OF INVENTION:  Endothelial Cells
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 760 Kb storage
;      COMPUTER:  DELL 486/50
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Displaywrite 3
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00445
;      FILING DATE:  19930105
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/820,011
;      FILING DATE:  06-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  ALX-101PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255 1400
;      TELEFAX:  (203) 254 1101
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  536 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Protein
;    HYPOTHETICAL:  No
;    FRAGMENT TYPE:  Complete Sequence
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapien
;    PUBLICATION INFORMATION:
;      AUTHORS:  Anderson, Stephen K.
;      AUTHORS:  Gibbs, Carol P.
;      AUTHORS:  Tanaka, Akio
;      AUTHORS:  Kung, Hsing-Jien
;      AUTHORS:  Fujita, Donald J.
;      TITLE:  Human Cellular src Gene:
;      TITLE:  Nucleotide Sequence and Derived Amino
;      TITLE:  Acid Sequence of the Region Coding for
;      TITLE:  the Carboxy-Terminal Two-Thirds of
;      TITLE:  pp60c-src
;      JOURNAL:  Molecular and Cellular Biology
;      VOLUME:  5
;      ISSUE:  5
;      PAGES:  1122-1129
;      DATE:  May, 1985
;    PUBLICATION INFORMATION:
;      AUTHORS:  Tanaka, Akio
;      AUTHORS:  Gibbs, Carol P.
;      AUTHORS:  Arthur, Richard R.
;      AUTHORS:  Anderson, Stephen K.
;      AUTHORS:  Kung, Hsing-Jien
;      AUTHORS:  Fujita, Donald J.
;      TITLE:  DNA Sequence Encoding the
;      TITLE:  Amino-Terminal Region of the Human c-src
;      TITLE:  Protein: Implications of Sequence
;      TITLE:  Divergence among src-Type Kinase
;      TITLE:  Oncogenes
;      JOURNAL:  Molecular and Cellular Biology
;      VOLUME:  7
;      ISSUE:  5
;      PAGES:  1978-1983
;      DATE:  May, 1987
PCT-US93-00445-4


alignment_scores:
            Quality: 2834.00                Length:    536
              Ratio:  5.287                   Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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Db  1363 gcacggcaaggtgccaagttccccatcaagtggacagcccccgaggcagccctctatggc 1422

Qy  1321 cgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccaca 1380
         || ||||||||||||||| || |||||||||| |||||||||||||||||| |||||
Db  1423 cggttcaccatcaagtcggatgtctggtccttcggcatcctgctgactgagctgaccacc 1482

Qy  1381 aagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcgg 1440
         ||||| |||||||| ||||| |||||||| ||| | |||||||||||||||||||| ||
Db  1483 aagggccgggtgccatacccagggatggtcaacagggaggtgctggaccaggtggagagg 1542

Qy  1441 ggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccag 1500
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Db  1543 ggctaccgcatgccctgcccgcccgagtgccccgagtcgctgcatgacctcatgtgccag 1602

Qy  1501 tgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggag 1560
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Db  1603 tgctggcggagggaccctgaggagcggcccactttgagtacctgcaggccttcctggag 1662

Qy  1561 gactacttcacgtccaccgagccccagtaccagcccggggagaaacctctag 1611
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Db  1663 gactacttcacctcgacagagccccagtaccagcctggagagaacctatag 1713


RESULT  4
AAH28357
ID  AAH28357 standard; cDNA; 1759 BP.
XX
AC  AAH28357;
XX
DT  05-SEP-2001  (first entry)
XX
DE  Nucleotide sequence of chicken tyrosine kinase protein Src.
XX
KW  Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KW  myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KW  diabetic retinopathy; inflammatory disease; infection; arthritis;
KW  adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW  diabetic retinopathy; psoriasis; neovascular glaucoma;
KW  capillary proliferation; osteoporosis; cancer; ss.
XX
OS  Gallus sp.
XX
FH  Key             Location/Qualifiers
FT  CDS             112..1713
FT                  /*tag= a
FT                  /product= "Src"
XX
PN  WO200145751-A1.
XX
PD  28-JUN-2001.
XX
PF  22-DEC-2000; 2000WO-US35396.
XX
PR  22-DEC-1999;   99US-0470881.
PR  29-MAR-2000; 2000US-0538248.
XX
PA  (SCRI ) SCRIPPS RES INST.
XX
PI  Cheresh DA,  Eliceiri B,  Paul R;
XX
DR  WPI; 2001-417982/44.
DR  P-PSDB; AAB84661.
XX
PT  Modulating vascular permeability in tissues, including inflamed tissue,
PT  tissues associated with stroke, myocardial infarction, by contacting
PT  the tissue with tyrosine kinase protein Src, Yes or their modified
PT  forms -
XX
PS  Disclosure; Fig 1; 133pp; English.
XX
CC  The specification describes a method for modulating vascular
CC  permeability in a tissue suffering from a disease condition. The method
CC  comprises contacting the tissue with a pharmaceutical composition
CC  comprising tyrosine kinase protein Src, Yes or their mixtures or
CC  nucleic acid expressing them. The method is useful for modulating
CC  vascular permeability in tissues, including inflamed tissue, tissues
CC  associated with stroke, myocardial infarction or other blockage of
CC  normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
CC  and similar tissues. Pathologies which may be treated include include
CC  trauma to blood vessels, and other systemic pathological events such as
CC  atherosclerosis, diabetic retinopathy, inflammatory disease due to
CC  infection by microbial agents and arthritis. Other diseases which can
CC  be treated include adult respiratory distress syndrome (ARDS), rheumatoid
CC  arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
CC  capillary proliferation in atherosclerotic plaques and osteoporosis and
CC  cancer associated disorders such as solid tumours, solid tumour
CC  metastases, angiofibromas and hemangiomas. The present sequence
CC  encodes chicken Src, and is used in the method of the invention.
XX
SQ  Sequence 1759 BP; 370 A; 554 C; 533 G; 302 T; 0 other;


  Query Match             75.6%;  Score 1218.2;  DB 22;  Length 1759;
  Best Local Similarity   85.3%;  Pred. No. 1.4e-220;
  Matches 1374;  Conservative    0;  Mismatches  228;  Indels    9;  Gaps    1;

Qy      1 atgggtagcaacaagagcaagcccaaggatgccagccagcggcgccgcagcctggagccc 60
          ||||| |||| |||||||||||||||||  |||||||||| || ||||||||||||||
Db    112 atggggagcagcaagagcaagcccaaggaccccagccagcgccggcgcagcctggagcca 171

Qy     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120
           |||| | |   ||| |         || |  ||||| |||||||||||||||| ||||
Db    172 cccgacagcacccaccac---------gggggattcccagcctcgcagacccccaacaag 222

Qy    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgcccccgcggccgccgag 180
           |||| |  |||||   ||||||  |||||||    |||| |   ||| |||| |||||
Db    223 acagcagcccccgacacgcaccgcaccccccagccgctcctttgggaccgtggccaccgag 282

Qy    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240
          |||||||| ||||| ||||||||| | || |||||||| || || |||||| | || ||
Db    283 cccaagctcttcgggggcttcaacacttctgacaccgttacgtcgccgcagcgtgccggg 342

Qy    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300
           | ||||| || || || ||||| || ||||| ||||| ||||| |||||  |||| ||
Db    343 gcactggctggcggcgtcaccactttcgtggctctctacgactacgagtcccggactgaa 402

Qy    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagac 360
          || ||| |||||||||||||||| || || || ||||||||||||||||||| || |||
Db    403 acggacttgtccttcaagaaaggagaacgcctgcagattgtcaacaacacggaaggtgac 462

Qy    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420
          |||||||||| || || ||||  |||||||||| |||||||||||||| ||||| ||
Db    463 tggtggctggctcattccctcactacaggacagacgggctacatccccagtaactatgtc 522

Qy    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480
          |||||||| |||||||||||||||| |||||||| ||||| |||||||| | ||||||
Db    523 gcgccctcagactccatccaggctgaagagtggtactttgggaagatcactcgtcgggag 582

Qy    481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540
          || |||||| | |||||||  | || |||||  | || |||||| | || || || ||
Db    583 tccgagcggctgctgctcaaccccgaaaaccccccggggaaccttcttggtccgggagagc 642

Qy    541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600
          ||||| || |||||||||| |||||||| || |||||||| ||||||||||||||| |||
Db    643 gagacgacaaaaggtgcctattgcctctccgtttctgactttgacaacgccaaggggctc 702

Qy    601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    703 aatgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcacgc 762

Qy    661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720
          || ||||||| ||||||||||||||||||||||||||||||||||| || |||||| ||
Db    763 acacagttcagcagcctgcagcagctggtggcctactactccaaacatgctgatggcttg 822

Qy    721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780
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Query Match           75.5%;  Score 1216.6;  DB 5;  Length 1602;
Best Local Similarity 85.2%;  Pred. No. 5.9e-238;
Matches 1373;  Conservative    0;  Mismatches  229;  Indels    9;  Gaps    1;

Qy      1 atgggtagcaacaagagcaagcccaaggatgccagccagcggcgccgcagcctggagccc 60
          |||||  ||||  ||||||||||||||||||  ||||||||||  ||  ||||||||||||||
Db      1 ATGGGGAGCAGCAAGAGCAAGCCCAAGGACCCCAGCCAGCGCCGGCGCAGCCTGGAGCCA 60

Qy     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120
          ||||  |  |   |||  |          ||  |  |||||  ||||||||||||||||  ||||
Db     61 CCCGACAGCACCCACCAC---------GGGGGATTCCCAGCCTCGCAGACCCCCAACAAG 111

Qy    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgcccccgcggccgccgag 180
          ||||  |  |||||   ||||||  |||||||    ||||  |   |||  |||| |||||
Db    112 ACAGCAGCCCCCGACACGCACCGCACCCCCAGCCGCTCCTTTGGGACCGTGGCCACCGAG 171

Qy    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240
          ||||||||  |||||  ||||||||  |  ||  ||||||||  ||  ||  ||||||  |  ||  ||
Db    172 CCCAAGCTCTTCGGGGGCTTCAACACTTCTGACACCGTTACGTCGCCGCAGCGTGCCGGG 231

Qy    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300
          |  |||||  ||  ||  ||  |||||  ||  |||||  |||||  |||||  ||||  ||
Db    232 GCACTGGCTGGCGGCGTCACCACTTTCGTGGCTCTCTACGACTACGAGTCCCGGACTGAA 291

Qy    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagac 360
          ||  |||  ||||||||||||||||  ||  ||  ||  ||||||||||||||||||||  ||  |||
Db    292 ACGGACTTGTCCTTCAAGAAAGGAGAACGCCTGCAGATTGTCAACAACACGGAAGGTGAC 351

Qy    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420
          ||||||||||  ||  ||  ||||  ||||||||||  ||||||||||||||  |||||  ||
Db    352 TGGTGGCTGGCTCATTCCCTCACTACAGGACAGACGGGCTACATCCCCAGTAACTATGTC 411

Qy    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480
          ||||||||  ||||||||||||||||||  ||||||||  |||||  ||||||||  |  ||||||
Db    412 GCGCCCTCAGACTCCATCCAGGCTGAAGAGTGGTACTTTGGGAAGATCACTCGTCGGGAG 471

Qy    481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540
          ||  ||||||  |  ||||||||  |  ||  |||||  |  ||  ||||||  |  ||  ||  ||  ||
Db    472 TCCGAGCGGCTGCTGCTCAACCCCGAAAACCCCCGGGGAACCTTCTTGGTCCGGGAGAGC 531

Qy    541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600
          |||||  ||  ||||||||||  ||||||||  ||  ||||||||  ||||||||||||||  |||
Db    532 GAGACGACAAAAGGTGCCTATTGCCTCTCCGTTTCTGACTTTGACAACGCCAAGGGGCTC 591

Qy    601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db    592 AATGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCACGC 651

Qy    661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720
          ||  |||||||  ||||||||||||||||||||||||||||||||||||||||  ||||||  ||
Db    652 ACACAGTTCAGCAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACATGCTGATGGCTTG 711

Qy    721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780
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Db    712 TGCCACCGCCTGACCAACGTCTGCCCCACGTCCAAGCCCCAGACCCAGGGACTCGCCAAG 771

Qy    781 gatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgc 840
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Db    772 GACGCGTGGGAAATCCCCCGGGAGTCGCTGCGGCTGGAGGTGAAGCTGGGGCAGGGCTGC 831

Qy    841 tttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctg 900
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Db    832 TTTGGAGAGGTCTGGATGGGGACCTGGAACGGCACCACCAGAGTGGCCATAAAGACTCTG 891

Qy    901 aagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctg 960
          |||||  ||||  |||||  ||  ||||||||||||||||||  |||||  ||  ||||||||||
Db    892 AAGCCCGGCAACATGTCCCCGGAGGCCTTCCTGCAGGAAGCCCAAGTGATGAAGAAGCTC 951

Qy    961 aggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtc 1020
          ||||||||||||||||  |||  ||||  ||  |||||  ||  ||  ||||||||  |||||||||
Db    952 CGGCATGAGAAGCTGGTTCAGCTGTACGCAGTGGTGTCGGAAGAGCCCATCTACATCGTC 1011

Qy   1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtac 1080
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Db   1012 ACTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCTGAAGGGAGAGATGGGCAAGTAC 1071

Qy   1081 ctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtg 1140
          ||||||||||  |||||  ||  ||||||||||||||  ||  ||  ||||||||  ||  |||
Db   1072 CTGCGGCTGCCACAGCTCGTCGATATGGCTGCTCAGATTGCATCCGGCATGGCCTATGTG 1131

Qy   1141 gagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaac 1200
          |||  ||||||||||||||  |||||  |||||  ||  ||  ||||||||||||||||||  ||||||
Db   1132 GAGAGGATGAACTACGTGCACCGAGACCTGCGGGCGGCCAACATCCTGGTGGGGGAGAAC 1191

Qy   1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260
          ||||||||||  |||||  ||||||||||||||  ||  |||||  ||  |||||  ||||||||
Db   1192 CTGGTGTGCAAGGTGGCTGACTTTGGGCTGGCACGCCTCATCGAGGACAACGAGTACACA 1251

Qy   1261 gcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggc 1320
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Db   1252 GCACGGCAAGGTGCCAAGTTCCCCATCAAGTGGACAGCCCCCGAGGCAGCCCTCTATGGC 1311

Qy   1321 cgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccaca 1380
          ||  ||||||||||||||||  ||  ||||||||||  ||||||||||||||||||  |||||
Db   1312 CGGTTCACCATCAAGTCGGATGTCTGGTCCTTCGGCATCCTGCTGACTGAGCTGACCACC 1371

Qy   1381 aagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcgg 1440
          |||||  ||||||||  |||||  ||||||||  |||  |  ||||||||||||||||||||  ||
Db   1372 AAGGGCCGGGTGCCATACCCAGGGATGGTCAACAGGGAGGTGCTGGACCAGGTGGAGAGG 1431

Qy   1441 ggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccag 1500
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Db   1432 GGCTACCGCATGCCCTGCCCGCCCGAGTGCCCCGAGTCGCTGCATGACCTCATGTGCCAG 1491

Qy   1501 tgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggag 1560
          ||||||||||  |||  ||||||||||||||||||  ||  ||||||||||||||||||||||||
Db   1492 TGCTGGCGGAGGGACCCTGAGGAGCGGCCCACTTTTGAGTACCTGCAGGCCTTCCTGGAG 1551

Qy   1561 gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag 1611
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Db   1552 GACTACTTCACCTCGACAGAGCCCCAGTACCAGCCTGGAGAGAACCTATAG 1602
```

```
RESULT   5
PCT-US93-06251-83
;  Sequence 83, Application PC/TUS9306251
;  GENERAL INFORMATION:
;     APPLICANT:  Wickstrom, Eric and Rife, Jason P.
;     TITLE OF INVENTION:  Trivalent Synthesis of Oligonucleotides Containing
;     TITLE OF INVENTION:  Stereospecific Alkylphosphonates and Arylphosphonates
;     NUMBER OF SEQUENCES:  93
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;       STREET:  400 Garden City Plaza
;       CITY:  Garden City
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  11530
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/06251
;       FILING DATE:  19930630
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DiGiglio, Frank S.
;       REGISTRATION NUMBER:  31,346
;       REFERENCE/DOCKET NUMBER:  8586
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  516-742-4343
;       TELEFAX:  516-742-4366
;       TELEX:  230 901 SANS UR
```

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Db    472 tccgagcggctgctgctcaaccccgaaaaccccccggggaaccttcttggtccgggagagc 531

Qy    541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600
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Db    532 gagacgacaaaaggtgcctattgcctctccgtttctgactttgacaacgccaaggggctc 591

Qy    601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    592 aatgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcacgc 651

Qy    661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720
          || ||||||| |||||||||||||||||||||||||||||||||| || |||||| ||
Db    652 acacagttcagcagcctgcagcagctggtggcctactactccaaacatgctgatggcttg 711

Qy    721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780
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Db    712 tgccaccgcctgaccaacgtctgccccacgtccaagccccagacccagggactcgccaag 771

Qy    781 gatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgc 840
          || || ||||| ||||| |||||||||||||||||||||||| |||||||| |||||||||
Db    772 gacgcgtgggaaatcccccgggagtcgctgcggctggaggtgaagctggggcagggctgc 831

Qy    841 tttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctg 900
          ||||| ||||| |||||||||||||||||||| |||||||| |||||||| || || |||
Db    832 tttggagaggtctggatggggacctggaacggcaccaccagagtggccataaagactctg 891

Qy    901 aagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctg 960
          ||||| ||||  ||||| || |||||||||||||||||| ||||| || ||||||||||
Db    892 aagcccggcaacatgtccccggaggccttcctgcaggaagcccaagtgatgaagaagctc 951

Qy    961 aggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtc 1020
          |||||||||||||||| ||| |||| || ||||| || || |||||||| |||||||||
Db    952 cggcatgagaagctggttcagctgtacgcagtggtgtcggaagagcccatctacatcgtc 1011

Qy    1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggggagacaggcaagtac 1080
           || |||||||||||||||||||  | |||||| || || ||||| ||||  |||||||||
Db    1012 actgagtacatgagcaaggggagcctcctggatttcctgaagggagagatgggcaagtac 1071

Qy    1081 ctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtg 1140
           |||||||||||| ||||| || || |||||||||||||| || || |||||||| || |||
Db    1072 ctgcggctgccacagctcgtcgatatggctgctcagattgcatccggcatggcctatgtg 1131

Qy    1141 gagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaac 1200
           ||| |||||||||||||| ||||| ||||| || || |||||||||||||||| ||||||
Db    1132 gagaggatgaactacgtgcaccgagacctgcgggcggccaacatcctggtgggggagaac 1191

Qy    1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260
           |||||||||||| ||||| |||||||||||||| || ||||| || ||||| ||||||||
Db    1192 ctggtgtgcaaggtggctgactttgggctggcacgcctcatcgaggacaacgagtacaca 1251

Qy    1261 gcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggc 1320
           || |||||||||||||| |||||||||||||||||| || || || || ||||||||||||
Db    1252 gcacggcaaggtgccaagttccccatcaagtggacagcccccgaggcagccctctatggc 1311

Qy    1321 cgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccaca 1380
           || |||||||||||||||| || |||||||||||| ||||||||||||||||| |||||
Db    1312 cggttcaccatcaagtcggatgtctggtccttcggcatcctgctgactgagctgaccacc 1371

Qy    1381 aagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcgg 1440
           ||||| |||||||| ||||| |||||||| ||| | ||||||||||||||||||||| ||
Db    1372 aagggccgggtgccatacccagggatggtcaacagggaggtgctggaccaggtggagagg 1431

Qy    1441 ggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccag 1500
           |||||||| |||||||||||||| ||||| |||||||| ||||| ||||||||||||||||
Db    1432 ggctaccgcatgccctgcccgcccgagtgccccgagtcgctgcatgacctcatgtgccag 1491

Qy    1501 tgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggag 1560
           |||||||||| ||| |||||||||||||||||| || ||||||||||||||||||||||||
Db    1492 tgctggcggagggaccctgaggagcggcccactttgagtacctgcaggccttcctggag 1551

Qy    1561 gactacttcacgtccaccgagccccagtaccagcccgggagaaacctctag 1611
           |||||||||| || || |||||||||||||||| || |||||||| |||
Db    1552 gactacttcacctcgacagagccccagtaccagcctggagagaacctatag 1602
```

RESULT 6
AAS87964
ID AAS87964 standard; cDNA; 1090 BP.
XX
AC AAS87964;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #23768.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG23777.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 23768; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1090 BP; 219 A; 331 C; 344 G; 196 T; 0 other;

Query Match 65.7%; Score 1058; DB 23; Length 1090;
Best Local Similarity 100.0%; Pred. No. 1.9e-190;
Matches 1058; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     554 gtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaacgtgaagcact 613
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 gtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaacgtgaagcact 60
```

PCT-US93-06251-77

Query Match 42.8%; Score 689.4; DB 5; Length 2647;
Best Local Similarity 69.6%; Pred. No. 3.2e-131;
Matches 952; Conservative 0; Mismatches 406; Indels 9; Gaps 1;

```
Qy    253 ggagtgaccacctttgtggccctctatgactatgagtctaggacggagacagacctgtcc 312
          ||||||||  ||||||||||||| ||||||||||  |  |||| ||    ||||||
Db    826 GGAGTGACACTCTTTGTGGCCCTTTATGACTATGAAGCACGGACAGAAGATGACCTGAGT 885

Qy    313 ttcaagaaaggcgagcggctccagattgtcaacaacacggagggagactggtggctggcc 372
          ||  | ||||| ||     | || ||  | |||| | |||| ||||| ||||||   |||
Db    886 TTTCACAAAGGAGAAAAATTTCAAATATTGAACAGCTCGGAAGGAGATTGGTGGGAAGCC 945

Qy    373 cactcgctcagcacaggacagacaggctacatccccagcaactacgtggcgccctccgac 432
          | |||  | |  || ||| ||||||| ||||| |||||||| || ||||| ||    |||
Db    946 CGCTCCTTGACAACTGGAGAGACAGGTTACATTCCCAGCAATTATGTGGCTCCAGTTGAC 1005

Qy    433 tccatccaggctgaggagtggtattttggcaagatcaccagacgggagtcagagcggtta 492
          || |||||||| || |||||||| ||||| ||  |  | ||   ||  | |||||
Db   1006 TCTATCCAGGCAGAAGAGTGGTACTTTGGAAAACTTGGCCGAAAAGATGCTGAGCGACAG 1065

Qy    493 ctgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagtgagaccacgaaa 552
          ||  |       |  ||||| ||||| ||||| ||  | || || ||||| ||||| |||
Db   1066 CTATTGTCCTTTGGAAACCCAAGAGGTACCTTTCTTATCCGCGAGAGTGAAACCACCAAA 1125

Qy    553 ggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaacgtgaagcac 612
          ||||||||  |  || ||  |   ||| |  ||  |    || ||   | | || || ||
Db   1126 GGTGCCTATTCACTTTCTATCCGTGATTGGGATGATATGAAAGGAGACCATGTCAAACAT 1185

Qy    613 tacaagatccgcaagctggacagcggcggcttctacatcacctcccgcacccagttcaac 672
          || || || ||||| || ||||  || || | |||||| ||| ||||  |||||||  |
Db   1186 TATAAAATTCGCAAACTTGACAATGGTGGATACTACATTACCACCCGGGCCCAGTTTGAA 1245

Qy    673 agcctgcagcagctggtggcctactactccaaacacgccgatggcctgtgccaccgcctc 732
          |  || |||||||| ||     | |||||  |    || |  || || |||  ||||||
Db   1246 ACACTTCAGCAGCTTGTACAACATTACTCAGAGAGAGCTGCAGGTCTCTGCTGCCGCCTA 1305

Qy    733 accaccgtgtgccccacgtccaagccgcagactcagggcctg---------gccaaggat 783
                || | ||     | |||   |  |   |  |||          |||| |||
Db   1306 GTAGTTCCCTGTCACAAAGGGATGCCAAGGCTTACCGATCTGTCTGTCAAAACCAAAGAT 1365

Qy    784 gcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgcttt 843
          | |||||| |||||||| || || |||| | ||       |  |||||  | ||    |||
Db   1366 GTCTGGGAAATCCCTCGAGAATCCCTGCAGTTGATCAAGAGACTGGGAAATGGGCAGTTT 1425

Qy    844 ggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaag 903
          || || || |||||||| |||||||| || | ||| |  || ||||| || || || ||
Db   1426 GGGGAAGTATGGATGGGTACCTGGAATGGAAACACAAAAGTAGCCATAAAGACTCTTAAA 1485

Qy    904 cctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgagg 963
          || ||||| ||||| || ||  | ||||| |||| || ||| ||||||||||||||| |
Db   1486 CCAGGCACAATGTCCCCCGAATCATTCCTTGAGGAAGCGCAGATCATGAAGAAGCTGAAG 1545

Qy    964 catgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtcacg 1023
          || || |||||||| ||| | ||||| ||||| || ||||||||||| ||||||||||
Db   1546 CACGACAAGCTGGTCCAGCTCTATGCAGTGGTGTCTGAGGAGCCCATCTACATCGTCACC 1605

Qy    1024 gagtacatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtacctg 1083
          ||||| |||| ||| || ||||| ||||| ||  | || |  |    ||| |    |||
Db   1606 GAGTATATGAACAAAGGAAGTTTACTGGATTTCTTAAAAGATGGAGAAGGAAGAGCTCTG 1665

Qy    1084 cggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggag 1143
            | ||  | || |||||||||| || ||| | ||  |||| ||||| ||| | |||
Db   1666 AAATTACCAAATCTTGTGGACATGGCAGCACAGGTGGCTGCAGGAATGGCTTACATCGAG 1725

Qy    1144 cggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaacctg 1203
          || ||||| ||  ||||  | || || ||  |||| ||||| || |||||  |    ||
Db   1726 CGCATGAATTATATCCATAGAGATCTGCGATCAGCAAACATTCTAGTGGGGAATGGACTC 1785

Qy    1204 gtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacggcg 1263
            | |||||  | || ||||| ||  |||| ||  | || ||||||||||||||||| ||
```

```
Db    1786 ATATGCAAGATTGCTGACTTCGGATTGGCCCGATTGATAGAAGACAATGAGTACACAGCA 1845

Qy    1264 cggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggccgc 1323
             | |||||||| || |||||||||||||||||||| || || || ||||| || ||  |
Db    1846 AGACAAGGTGCAAAGTTCCCCATCAAGTGGACGGCCCCCGAGGCAGCCCTGTACGGGAGG 1905

Qy    1324 ttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccacaaag 1383
           ||||| |||||||| |||||||||| || || ||| | || || ||||   ||| ||
Db    1906 TTCACAATCAAGTCTGACGTGTGGTCTTTTGGAATCTTACTCACAGAGCTGGTCACCAAA 1965

Qy    1384 ggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcggggc 1443
           ||| | ||||| ||||| || |||   ||||| |||||||||| |||||||||| |||
Db    1966 GGAAGAGTGCCATACCCAGGCATGAACAACCGGGAGGTGCTGGAGCAGGTGGAGCGAGGC 2025

Qy    1444 taccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccagtgc 1503
           ||| |||||||||||||| ||| || |||   || ||||| || ||||||  ||| |||
Db    2026 TACAGGATGCCCTGCCCGCAGGACTGCCCCATCTCTCTGCATGAGCTCATGATCCACTGC 2085

Qy    1504 tggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggaggac 1563
           |||   ||||| |||| || || |||| || |||||| |||||  |||||||| |||
Db    2086 TGGAAAAAGGACCCTGAAGAACGCCCCACTTTTGAGTACTTGCAGAGCTTCCTGGAAGAC 2145

Qy    1564 tacttcacgtccaccgagccccagtaccagcccggggagaacctcta 1610
           ||||| ||  | || |||||||||||||| || || || ||||| ||
Db    2146 TACTTTACCGCGACAGAGCCCCAGTACCAACCTGGTGAAAACCTGTA 2192
```

RESULT 7
US-08-306-691B-40
; Sequence 40, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1804 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-306-691B-40

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Qy    808 ctgcggctggaggtcaagctgggccagggctgctttggcgaggtgtggatggggacctgg 867
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 ctgcggctggaggtcaagctgggccagggctgctttggcgaggtgtggatggggacctgg 513

Qy    868 aacggtaccaccagggtggccatcaaaaccctgaagcctggcacgatgtctccagaggcc 927
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 aacggtaccaccagggtggccatcaaaaccctgaagcctggcacgatgtctccagaggcc 573

Qy    928 ttcctgcaggaggcccaggtcatgaagaagctgaggcatgagaagctggtgcagttgtat 987
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 ttcctgcaggaggcccaggtcatgaagaagctgaggcatgagaagctggtgcagttgtat 633

Qy    988 gctgtggtttcagaggagcccatttacatcgtcacggagtacatgagcaaggggagtttg 1047
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 gctgtggtttcagaggagcccatttacatcgtcacggagtacatgagcaaggggagtttg 693

Qy   1048 ctggactttctcaaggggagacaggcaagtacctgcggctgcctcagctggtggacatg 1107
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 ctggactttctcaaggggagacaggcaagtacctgcggctgcctcagctggtggacatg 753

Qy   1108 gctgctcagatcgcctcaggcatggcgtacgtggagcggatgaactacgtccaccgggac 1167
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 gctgctcagatcgcctcaggcatggcgtacgtggagcggatgaactacgtccaccgggac 813

Qy   1168 cttcgtgcagccaacatcctggtgggagagaacctggtgtgcaaagtggccgactttggg 1227
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 cttcgtgcagccaacatcctggtgggagagaacctggtgtgcaaagtggccgactttggg 873

Qy   1228 ctggctcggctcattgaagacaatgagtacacggcgcggcaaggtgccaaattccccatc 1287
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 ctggctcggctcattgaagacaatgagtacacggcgcggcaaggtgccaaattccccatc 933

Qy   1288 aagtggacggctccagaagctgccctctatggccgcttcaccatcaagtcggacgtgtgg 1347
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 aagtggacggctccagaagctgccctctatggccgcttcaccatcaagtcggacgtgtgg 993

Qy   1348 tccttcgggatcctgctgactgagctcaccacaaagggacgggtgccctaccctgggatg 1407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 tccttcgggatcctgctgactgagctcaccacaaagggacgggtgccctaccctgggatg 1053

Qy   1408 gtgaaccgcgaggtgctggaccaggtggagcggggctaccggatgccctgcccgccggag 1467
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 gtgaaccgcgaggtgctggaccaggtggagcggggctaccggatgccctgcccgccggag 1113

Qy   1468 tgtcccgagtccctgcacgacctcatgtgccagtgctggcggaaggagcctgaggagcgg 1527
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 tgtcccgagtccctgcacgacctcatgtgccagtgctggcggaaggagcctgaggagcgg 1173

Qy   1528 cccaccttcgagtacctgcaggccttcctggaggactacttcacgtccaccgagccccag 1587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 cccaccttcgagtacctgcaggccttcctggaggactacttcacgtccaccgagccccag 1233

Qy   1588 taccagcccggggagaacctctag 1611
          |||||||||||||||||||||||
Db   1234 taccagcccggggagaacctctag 1257
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RESULT   8
AAS94859
ID   AAS94859 standard; DNA; 2433 BP.
XX
AC   AAS94859;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human DNA sequence #114 expressed during foam cell differentiation.
XX
KW   Human; foam cell differentiation; atherosclerosis; cerebral stroke;
KW   cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200177389-A2.
XX
PD   18-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US11128.
XX
PR   05-APR-2000; 2000US-195106P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Shiffman D,  Somogyi R,  Lawn R,  Seilhamer JJ,  Porter GJ,  Mikita T;
PI   Tai J;
XX
DR   WPI; 2002-010925/01.
XX
PT   Composition useful for diagnosis of conditions, disorders or diseases
PT   associated with atherosclerosis, comprises several polynucleotides that
PT   are differentially expressed in foam cell development -
XX
PS   Claim 1; Page 169; 315pp; English.
XX
CC   The present invention relates to the isolation of human polynucleotide
CC   sequences that are differentially expressed during foam cell
CC   differentiation. The polynucleotide sequences of the invention or a
CC   composition comprising these polynucleotides are useful as a high
CC   throughput method for detecting altered expression of one or more
CC   polynucleotides in a sample. The polynucleotides can be used in the
CC   diagnosis of disorders associated with foam cell development such as
CC   atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC   coronary artery disease. The polynucleotide sequences can also be used
CC   as PCR primers and probes. The polynucleotides of the invention are also
CC   useful in gene therapy. AAS94746-AAS95021 represent the human
CC   polynucleotide sequences of the invention which are differentially
CC   expressed during foam cell differentiation.
XX
SQ   Sequence 2433 BP; 547 A; 676 C; 687 G; 523 T; 0 other;
```

```
  Query Match             50.4%;  Score 811.2;  DB 24;  Length 2433;
  Best Local Similarity   73.9%;  Pred. No. 6.2e-144;
  Matches 1029;  Conservative    0;  Mismatches  363;  Indels    0;  Gaps    0;

Qy    220 acctccccgcagagggcgggcccgctggccggtggagtgaccacctttgtggccctctat 279
          |||   | |   ||  | | | |    |   ||| ||||||   ||  | ||||| |||
Db    267 accctgctgagtagccctgactctgcagggattggggtgaccctgttcattgccctgtat 326

Qy    280 gactatgagtctaggacggagacagacctgtccttcaagaaaggcgagcggctccagatt 339
          |||||||| || | || |||   |||||  ||||||  || ||||||  | |||| ||
Db    327 gactatgaggctcgaactgaggatgacctcaccttcaccaagggcgagaagttccacatc 386

Qy    340 gtcaacaacacggagggagactggtggctggcccactcgctcagcacaggacagacaggc 399
           | ||||| || || || |||||||||  ||| |  || ||||||  | ||| | || |||
Db    387 ctgaacaatactgaaggtgactggtgggaggctcggtctctcagctccggaaaaactggc 446

Qy    400 tacatccccagcaactacgtggcgcccctccgactccatccaggctgaggagtggtatttt 459
          | ||| ||||||||||||||||| ||    ||||| ||||| ||||| |||||||| |||
Db    447 tgcattcccagcaactacgtggcccctgttgactcaatccaagctgaagagtggtacttt 506

Qy    460 ggcaagatcaccagacgggagtcagagcggttactgctcaatgcagagaacccgagaggg 519
          || |||||    |||  |||  ||||| ||   |||||     |||  |||||    |||
Db    507 ggaaagattgggagaaaggatgcagagaggcagctgctttcaccaggcaacccccagggg 566

Qy    520 accttcctcgtgcgagaaagtgagaccacgaaaggtgcctactgcctctcagtgtctgac 579
          |||| ||| | || ||||| |||||||| |||||||||||||| ||| ||  |    |||
Db    567 gcctttctcattcgggaaagcgagaccaccaaaggtgcctactccctgtccatccgggac 626

Qy    580 ttcgacaacgccaagggcctcaacgtgaagcactacaagatccgcaagctggacagcggc 639
          |  ||  |  |||  |||    | |||||||| |||||||||||||| |||||||  |||
Db    627 tgggatcagaccagaggcgatcatgtgaagcattacaagatccgcaaactggacatgggc 686

Qy    640 ggcttctacatcacctcccgcacccagttcaacagcctgcagcagctggtggcctactac 699
          |||| ||||||||| | ||    |||||||||    ||||| ||||||||    |||||
Db    687 ggctactacatcaccacacgggttcagttcaactcggtgcaggagctggtgcagcactac 746
```

CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 565 AA;

alignment_scores:
Quality: 2408.50 Length: 550
Ratio: 4.946 Gaps: 3
Percent Similarity: 88.545 Percent Identity: 85.273

alignment_block:
US-09-444-711-1 x ABG23778 ..

gn seg 1/1 to: ABG23778 from: 1 to: 565

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  58 CCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCGCC..... 102
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  16 ProGluArgAlaValLeuGluSerArgGlyGlyAlaProAspThrProAr 32

 103 ..........TCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACC 142
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  32 gArgLeuHisSerPheThrGlnThrArgSerLeuSerProGlnAlaHisA 49

 143 GCGGCCCCAGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTC 192
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  49 laGlyProHisThrArgLeuHisProArgGlnGlyHisAlaHisMetArg 65

 193 GGAGGCTTCAACTCCTCGGACACC.................GTCACCTC 224
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  66 GlyGlyGlyArgValThrAspThrArgArgHisIleProAsnAlaAspVa 82

 225 CCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTGACCACCTTTGTGGCCC 274
      |||:::                :::|||||||||||||||||||||||||
  82 lProArgTyrLysLeuThrCysThrGlyGlyValThrThrPheValAlaL 99

 275 TCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAAAGGC 324
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  99 euTyrAspTyrGluSerArgThrGluThrAspLeuSerPheLysLysGly 115

 325 GAGCGGCTCCAGATTGTCAACAACACGGAGGGAGACTGGTGGCTGGCCCA 374
     ||||||||||||||||||||||||:::|||||||||||||||||||||||
 116 GluArgLeuGlnIleValAsnAsnThrLysGlyAspTrpTrpLeuAlaHi 132

 375 CTCGCTCAGCACAGGACAGACAGGCTACATCCCCAGCAACTACGTGGCGC 424
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 132 sSerLeuSerThrGlyGlnThrGlyTyrIleProSerAsnTyrValAlaP 149

 425 CCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGA 474
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 475 CGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTT 524
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 166 ArgGluSerGluArgLeuLeuLeuAsnAlaGluAsnProArgGlyThrPh 182

 525 CCTCGTGCGAGAAAGTGAGACCACGAAAGGTGCCTACTGCCTCTCAGTGT 574
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 182 eLeuValArgGluSerGluThrThrLysGlyAlaTyrCysLeuSerValS 199

 575 CTGACTTCGACAACGCCAAGGGCCTCAACGTGAAGCACTACAAGATCCGC 624
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 199 erAspPheAspAsnAlaLysGlyLeuAsnValLysHisTyrLysIleArg 215

 625 AAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGCACCCAGTTCAACAG 674
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 216 LysLeuAspSerGlyGlyPheTyrIleThrSerArgThrGlnPheAsnSe 232

 675 CCTGCAGCAGCTGGTGGCCTACTACTCC..................... 702
     |||||||||||||||||||||||||||
 232 rLeuGlnGlnLeuValAlaTyrTyrSerMetSerHisCysProProPheS 249

 703 .....................................AAACAC 708
                                          ||||||
 249 erAlaAlaGlyTrpTyrGlyGlyGlyCysProGluGluProGlnLysHis 265

 709 GCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCC 758
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 266 AlaAspGlyLeuCysHisArgLeuThrThrValCysProThrSerLysPr 282

 759 GCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGC 808
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 809 TGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATG 858
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 316 GlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeuLysProGl 332

 909 CACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGC 958
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 959 TGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCC 1008
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 366 IleTyrIleValThrGluTyrMetSerLysGlySerLeuLeuAspPheLe 382

1059 CAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGTGGACATGG 1108
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1109 CTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTC 1158
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 432 sLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAsnGluTyrT 449

1259 CGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCT 1308
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 449 hrAlaArgGlnGlyAlaLysProIleLysTrpThrAlaProGluAla 465

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 482 eLeuLeuThrGluLeuThrThrLysGlyArgValProTyrProGlyMetV 499

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 499 alAsnArgGluValLeuAspGlnValGluArgGlyTyrArgMetProCys 515

1459 CCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAGTGCTGGCG 1508
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Qy    488 ggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagtgagacca 547
Db    716 gattacttttgaatcctggaaatcaacgaggtattttcttagtaagagagagtgaaacaa 775

Qy    548 cgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaacgtga 607
Db    776 ctaaaggtgcttattccctttctattcgtgattgggatgagataaggggtgacaatgtga 835

Qy    608 agcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgcacccagt 667
Db    836 aacactacaaaattaggaaacttgacaatggtggatactatatcacaaccagagcacaat 895

Qy    668 tcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctgtgccacc 727
D     896 ttgatactctgcagaaattggtgaaacactacacagaacatgctgatggtttatgccaca 955

Qy    728 gcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaaggatgcct 787
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Qy    908 gcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcatg 967
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Qy    968 agaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtcacggagt 1027
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Qy   1028 acatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtacctgcggc 1087
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Qy   1088 tgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggagcgga 1147
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Qy   1568 tcacgtccaccgagccccagtaccagcccggggagaacctcta 1610
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RESULT 10
AAH28359
ID AAH28359 standard; cDNA; 4517 BP.
XX
AC AAH28359;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of human tyrosine kinase protein Yes.
XX
KW Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KW myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KW diabetic retinopathy; inflammatory disease; infection; arthritis;
KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW diabetic retinopathy; psoriasis; neovascular glaucoma;
KW capillary proliferation; osteoporosis; cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 208..1839
FT /*tag= a
FT /product= "Yes"
XX
PN WO200145751-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35396.
XX
PR 22-DEC-1999; 99US-0470881.
PR 29-MAR-2000; 2000US-0538248.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Cheresh DA, Eliceiri B, Paul R;
XX
DR WPI; 2001-417982/44.
DR P-PSDB; AAB84663.
XX
PT Modulating vascular permeability in tissues, including inflamed tissue,
PT tissues associated with stroke, myocardial infarction, by contacting
PT the tissue with tyrosine kinase protein Src, Yes or their modified
PT forms -
XX
PS Disclosure; Fig 12; 133pp; English.
XX
CC The specification describes a method for modulating vascular
CC permeability in a tissue suffering from a disease condition. The method
CC comprises contacting the tissue with a pharmaceutical composition
CC comprising tyrosine kinase protein Src, Yes or their mixtures or
CC nucleic acid expressing them. The method is useful for modulating
CC vascular permeability in tissues, including inflamed tissue, tissues
CC associated with stroke, myocardial infarction or other blockage of
CC normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
CC and similar tissues. Pathologies which may be treated include include
CC trauma to blood vessels, and other systemic pathological events such as
CC atherosclerosis, diabetic retinopathy, inflammatory disease due to
CC infection by microbial agents and arthritis. Other diseases which can
CC be treated include adult respiratory distress syndrome (ARDS), rheumatoid
CC arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
CC capillary proliferation in atherosclerotic plaques and osteoporosis and
CC cancer associated disorders such as solid tumours, solid tumour
CC metastases, angiofibromas and hemangiomas. The present sequence
CC encodes human Yes, and is used in the method of the invention.
XX

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 248 CysHisLysLeuThrThrValCysProThrValLysProGlnThrGlnGl 264

 771 CCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGG 820
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 264 yLeuAlaLysAspAlaTrpGluIleProArgGluSerLeuArgLeuGluV 281

 821 TCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGAAC 870
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 281 alLysLeuGlyGlnGlyCysPheGlyGluValTrpMetGlyThrTrpAsn 297

 871 GGTACCACCAGGGTGGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCC 920
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 298 GlyThrThrLysValAlaIleLysThrLeuLysProGlyThrMetMetPr 314

 921 AGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTGAGGCATGAGA 970
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 314 oGluAlaPheLeuGlnGluAlaGlnIleMetLysLysLeuArgHisAspL 331

 971 AGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTC 1020
     ||||||||   ||||||||||||||||||||||||||||||||||||||||
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 364 pGlyLysTyrLeuLysLeuProGlnLeuValAspMetAlaAlaGlnIleA 381

1121 CCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTCCACCGGGACCTT 1170
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 381 laAspGlyMetAlaTyrIleGluArgMetAsnTyrIleHisArgAspLeu 397

1171 CGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTGCAAAGTGGCCGA 1220
     ||||||||||||||||||||||||||||||||||||||||||:::|||||
 398 ArgAlaAlaAsnIleLeuValGlyGluAsnLeuValCysLysIleAlaAs 414

1221 CTTTGGGCTGGCTCGGCTCATTGAAGACAATGAGTACACGGCGCGGCAAG 1270
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 414 pPheGlyLeuAlaArgLeuIleGluAspAsnGluTyrThrAlaArgGlnG 431

1271 GTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGC 1320
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 431 lyAlaLysProIleLysTrpThrAlaProGluAlaAlaLeuTyrGly 447

1321 CGCTTCACCATCAAGTCGGACGTGTGGTCCTTCGGGATCCTGCTGACTGA 1370
     ||||||||||||||||||||||||||||||||||||||||   |||||
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1371 GCTCACCACAAAGGGACGGGTGCCCTACCCTGGGATGGTGAACCGCGAGG 1420
     ||||:::|||||||||||||||||||||||||||||||||||||||||||
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1421 TGCTGGACCAGGTGGAGCGGGGCTACCGGATGCCCTGCCCGCCGGAGTGT 1470
     |||||:::|||||||||||||||||||||||||||||||||      |||
 481 alLeuGluGlnValGluArgGlyTyrArgMetProCysProGlnGlyCys 497

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     ||||||||||||||:::||||||      ||||||:::|||:::||||::
 498 ProGluSerLeuHisGluLeuMetAsnLeuCysTrpLysLysAspProAs 514

1521 GGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGGAGGACTACTTCA 1570
     :|||||||||||||||||||:::|||:::|||||||||||||||||||||
 514 pGluArgProThrPheGluTyrIleGlnSerPheLeuGluAspTyrPheT 531

1571 CGTCCACCGAGCCCCAGTACCAGCCCGGGGAGAACCTC 1608
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 531 hrAlaThrGluProGlnTyrGlnProGlyGluAsnLeu 543

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:AAB84663

seq_documentation_block:

ID   AAB84663 standard; Protein; 543 AA.
XX
AC   AAB84663;
XX
DT   05-SEP-2001  (first entry)
XX
DE   Amino acid sequence of human tyrosine kinase protein Yes.
XX
KW   Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KW   myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KW   diabetic retinopathy; inflammatory disease; infection; arthritis;
KW   adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW   diabetic retinopathy; psoriasis; neovascular glaucoma;
KW   capillary proliferation; osteoporosis; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200145751-A1.
XX
PD   28-JUN-2001.
XX
PF   22-DEC-2000; 2000WO-US35396.
XX
PR   22-DEC-1999;   99US-0470881.
PR   29-MAR-2000; 2000US-0538248.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Cheresh DA,  Eliceiri B,  Paul R;
XX
DR   WPI; 2001-417982/44.
DR   N-PSDB; AAH28359.
XX
PT   Modulating vascular permeability in tissues, including inflamed tissue,
PT   tissues associated with stroke, myocardial infarction, by contacting
PT   the tissue with tyrosine kinase protein Src, Yes or their modified
PT   forms -
XX
PS   Disclosure; Fig 11; 133pp; English.
XX
CC   The specification describes a method for modulating vascular
CC   permeability in a tissue suffering from a disease condition. The method
CC   comprises contacting the tissue with a pharmaceutical composition
CC   comprising tyrosine kinase protein Src, Yes or their mixtures or
CC   nucleic acid expressing them. The method is useful for modulating
CC   vascular permeability in tissues, including inflamed tissue, tissues
CC   associated with stroke, myocardial infarction or other blockage of
CC   normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
CC   and similar tissues. Pathologies which may be treated include include
CC   trauma to blood vessels, and other systemic pathological events such as
CC   atherosclerosis, diabetic retinopathy, inflammatory disease due to
CC   infection by microbial agents and arthritis. Other diseases which can
CC   be treated include adult respiratory distress syndrome (ARDS), rheumatoid
CC   arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
CC   capillary proliferation in atherosclerotic plaques and osteoporosis and
CC   cancer associated disorders such as solid tumours, solid tumour
CC   metastases, angiofibromas and hemangiomas. The present sequence
CC   represents human Yes, and is used in the method of the invention.
XX
SQ   Sequence   543 AA;


alignment_scores:
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 Percent Similarity:  86.813   Percent Identity: 74.542

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CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4517 BP; 1437 A; 784 C; 955 G; 1341 T; 0 other;

ery Match 44.1%; Score 710.2; DB 23; Length 4517;
t Local Similarity 70.1%; Pred. No. 6.9e-125;
Matches 955; Conservative 0; Mismatches 408; Indels 0; Gaps 0;

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Db    596 aagcaagatcaatcgctacaggaaagaatggttatatcccgagcaattatgtagcgcctg 655

Qy    428 ccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggagtcagagc 487
          | || ||||| ||||| || || ||||||||||||||| ||    |||   ||  | ||
Db    656 cagattccattcaggcagaagaatggtattttggcaaaatggggagaaaagatgctgaaa 715

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Qy    548 cgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaacgtga 607
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Qy    668 tcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctgtgccacc 727
          |  | |  ||||||  |  |||||    |||||  |  |||| || |||||  | ||||||
Db    896 ttgatactctgcagaaattggtgaaacactacacagaacatgctgatggtttatgccaca 955

Qy    728 gcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaaggatgcct 787
            | || || ||||| || ||    || || |||||||| || || || || ||||| |
Db    956 agttgacaactgtgtgtccaactgtgaaacctcagactcaaggtctagcaaaagatgctt 1015

Qy    788 gggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgctttggcg 847
          |||| |||||||| || ||  |||| || ||||| || || || || || || || ||||
Db    1016 gggaaatccctcgagaatctttgcgactagaggttaaactaggacaaggatgtttcggcg 1075

Qy    848 aggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaagcctg 907
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Db    1076 aagtgtggatgggaacatggaatggaaccacgaaagtagcaatcaaaacactaaaaccag 1135

Qy    908 gcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcatg 967
          | || |||   ||||| || ||||| || || || ||| | ||||| ||  | || ||||
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Qy    968 agaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtcacggagt 1027
          | || || || |   | |||||||| ||||| || || || |||||||| ||||| || |
Db    1196 ataaacttgttccactatatgctgttgtttctgaagaaccaatttacattgtcactgaat 1255

Qy    1028 acatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtacctgcggc 1087
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Db    1256 ttatgtcaaaaggaagcttattagatttccttaaggaaggagatggaaagtatttgaagc 1315

Qy    1088 tgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggagcgga 1147
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Db    1316 ttccacagctggttgatatggctgctcagattgctgatggtatggcatatattgaaagaa 1375

Qy    1148 tgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaacctggtgt 1207
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Db    1376 tgaactatattcaccgagatcttcgggctgctaatattcttgtaggagaaaatcttgtgt 1435

Qy    1208 gcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacggcgcggc 1267
           ||||| | || |||||||  | || ,|| | |||||||||||||| ||||| ||  | |
Db    1436 gcaaaatagcagactttggtttagcaaggttaattgaagacaatgaatacacagcaagac 1495

Qy    1268 aaggtgccaaattccccatcaagtggacggctccagaagctgcccctctatggccgcttca 1327
           ||||||| ||||| || ||||| ||||| ||||| |||||||| || ||||| || || |
Db    1496 aaggtgcaaaatttccaatcaaatggacagctcctgaagctgcactgtatggtcggttta 1555

Qy    1328 ccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccacaaagggac 1387
           | || ||||| || || ||||| || || || ||||  || || ||    |||||||| |
Db    1556 caataaagtctgatgtctggtcatttggaattctgcaaacagaactagtaacaaagggcc 1615

Qy    1388 gggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcggggctacc 1447
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Qy    1568 tcacgtccaccgagcccccagtaccagcccggggagaacctcta 1610
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RESULT 12
AAZ46491
ID AAZ46491 standard; DNA; 2032 BP.
XX
AC AAZ46491;
XX
DT 13-MAR-2000 (first entry)
XX
DE PKA substrate, Src-family protein encoding DNA.
XX
KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW kinase substrate; immunosuppressive disorder; proliferative disease;
KW HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW systemic lupus erythematosus; Src-family; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 52..1581
FT /*tag= a
XX
PN WO9962315-A2.
XX
PD 02-DEC-1999.
XX
PF 27-MAY-1999; 99WO-GB01680.
XX
PR 27-MAY-1998; 98NO-0002419.
PR 30-DEC-1998; 98US-0114240.
XX
PA (LAUR-) LAURAS AS.
PA (JONE/) JONES E L.

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XX
OS   Homo sapiens.
XX
PN   WO9935290-A1.
XX
PD   15-JUL-1999.
XX
PF   07-JAN-1999;   99WO-US00297.
XX
PR   08-JAN-1998;   98US-0003944.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Chen H,  Freimer NB;
XX
DR   WPI; 1999-444203/37.
DR   N-PSDB; AAX90200.
XX
PT   Detection of a genetic mutation in the yes1 gene, useful for
PT   diagnosis of a yes1 mediated neuropsychiatric disorder in a human
XX
PS   Disclosure; Fig 1; 110pp; English.

     The present invention describes a method for detecting a genetic
CC   mutation in the yes1 gene for the diagnosis of a yes1 mediated
CC   neuropsychiatric disorder in a human. The method comprises detecting the
CC   presence or absence of a genetic mutation in the yes1 gene of the
CC   subject, where the genetic mutation is a substitution, insertion or a
CC   deletion and results in the production of a yes1 protein having an amino
CC   acid sequence other than the wild-type yes1 amino acid sequence and the
CC   presence of the genetic mutation identifies a subject that has or is at
CC   risk for developing a yes1 mediated neuropsychiatric disorder. Compounds
CC   that bind to the yes1 protein, alter the amount of the protein, or alter
CC   the activity of the yes1 gene product, are useful for treating a yes1
CC   mediated neuropsychiatric disorder. The disorders include Huntington's
CC   disease, Parkinson's disease, and especially bipolar-affected disorder
CC   (BAD) also known as bipolar mood disorder (BP) or manic-depressive
CC   illness. The method distinguishes neuropsychiatric disorders from
CC   neurological disorders, which enables more accurate evaluation and
CC   prescription of medical treatment. The present sequence represents the
CC   human yes1 protein sequence.
XX
SQ   Sequence   543 AA;


alignment_scores:
            Quality: 2115.50              Length:    546
              Ratio:  4.473                Gaps:      4
 Percent Similarity:  86.630   Percent Identity: 74.359

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   -09-444-711-1 x AAY24421   ..

 Align seg 1/1  to: AAY24421  from: 1  to: 543

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         ||||||      |||||||||      |||:::   :::   :::   ||
       1 MetGlyCysIleLysSerLysGluAsnLysSerProAlaIleLysTyrAr 17

      48 CAGCCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGG......GGCG 91
         |      :::      |||   |||      :::   :::      ||||
      17 gProGluAsnThrProGluProValSerThrSerValSerHisTyrGlyA 34

      92 CTTTCCCCGCCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCAC 141
         ||   |||::::::   :::|||         :::|||||
      34 laGluProThrThrValSerProCysProSerSerSerAla..... 47

     142 CGCGGCCCCAGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCC..... 183
         :::|||   ::::::   |||:::      :::      |||
      48 LysGlyThrAlaValAsnPheSerSerLeuSerMetThrProPheGlyGl 64

     184 .............AAGCTGTTCGGAGGCTTCAACTCCTCGGACACCGTCA 220
                          |||||||||   :::|||||||   :::|||:

      64 ySerSerGlyValThrProPheGlyGlyAlaSerSerSerPheSerValV 81

     221 CCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTGACCACCTTTGTG 270
         ::      :::      :::   |||:::||||||||||||   ||||||
      81 alProSerSerTyrProAlaGlyLeuThrGlyGlyValThrIlePheVal 97

     271 GCCCTCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAA 320
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      98 AlaLeuTyrAspTyrGluAlaArgThrThrGluAspLeuSerPheLysLy 114

     321 AGGCGAGCGGCTCCAGATTGTCAACAACACGGAGGGAGACTGGTGGCTGG 370
         |||||||||:::||||||:::|||||||||||||||||||||||||   |
     114 sGlyGluArgPheGlnIleIleAsnAsnThrGluGlyAspTrpTrpGluA 131

     371 CCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCCAGCAACTACGTG 420
         ||:::|||:::::::||||||:::::::|||||||||||||||||||||||
     131 laArgSerIleAlaThrGlyLysAsnGlyTyrIleProSerAsnTyrVal 147

     421 GCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCAC 470
         ||||||:::|||||||||||||||||||||||||||||||||||||:::
     148 AlaProAlaAspSerIleGlnAlaGluGluTrpTyrPheGlyLysMetGl 164

     471 CAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGA 520
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     164 yArgLysAspAlaGluArgLeuLeuLeuAsnProGlyAsnGlnArgGlyI 181

     521 CCTTCCTCGTGCGAGAAAGTGAGACCACGAAAGGTGCCTACTGCCTCTCA 570
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     181 lePheLeuValArgGluSerGluThrThrLysGlyAlaTyrSerLeuSer 197

     571 GTGTCTGACTTCGACAACGCCAAGGGCCTCAACGTGAAGCACTACAAGAT 620
         :::   |||:::|||:::   :::|||   ||||||||||||||||||||
     198 IleArgAspTrpAspGluIleArgGlyAspAsnValLysHisTyrLysIl 214

     621 CCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGCACCCAGTTCA 670
         |||||||||||||:::||||||:::|||||||||:::|||:::||||||:
     214 eArgLysLeuAspAsnGlyGlyTyrTyrIleThrThrArgAlaGlnPheA 231

     671 ACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG 720
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     231 spThrLeuGlnLysLeuValLysHisTyrThrGluHisAlaAspGlyLeu 247

     721 TGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGG 770
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     248 CysHisLysLeuThrThrValCysProThrValLysProGlnThrGlnGl 264

     771 CCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGG 820
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     264 yLeuAlaLysAspAlaTrpGluIleProArgGluSerLeuArgLeuGluV 281

     821 TCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGAAC 870
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     281 alLysLeuGlyGlnGlyCysPheGlyGluValTrpMetGlyThrTrpAsn 297

     871 GGTACCACCAGGGTGGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCC 920
         |||||||||:::||||||||||||||||||   ||||||||||||   ||
     298 GlyThrThrLysValAlaIleLysThrLeuCysProGlyThrMetMetPr 314

     921 AGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTGAGGCATGAGA 970
         ||||||||||||||||||||||||:::|||||||||||||||||||:::|
     314 oGluAlaPheLeuGlnGluAlaGlnIleMetLysLysLeuArgHisAspL 331

     971 AGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTC 1020
         ||||||||   ||||||||||||||||||||||||||||||||||||||
     331 ysLeuValProLeuTyrAlaValValSerGluGluProIleTyrIleVal 347

    1021 ACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTTTCTCAAGGGGGAGAC 1070
         ||||||:::|||||||||||||||||||||||||||||||||||||||||
     348 ThrGluPheMetSerLysGlySerLeuLeuAspPheLeuLysGluGlyAs 364

    1071 AGGCAAGTACCTGCGGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCG 1120
         ||||||||||||:::||||||||||||||||||||||||||||||||||||
     364 pGlyLysTyrLeuLysLeuProGlnLeuValAspMetAlaAlaGlnIleA 381
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PN WO9725860-A1.
XX
PD 24-JUL-1997.
XX
PF 13-JAN-1997; 97WO-US00582.
XX
PR 19-JAN-1996; 96US-0010262.
XX
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.
XX
PI England JM, Halpern MS;
XX
DR WPI; 1997-384993/35.
XX
PT Proto-oncogene immunogen - used in vaccine for the prevention and
PT treatment of cancer
XX
PS Disclosure; Page 69-70; 81pp; English.
XX
CC This sequence represents the human c-yes-2 cognate transgene (CTG).
CC Deletion of amino acids 438-441 of the encoded protein renders the CTG
CC non-transforming. This sequence can be used in the cellular immunogen of
CC the invention. The cellular immunogen of the invention is for immunising
CC against the product of a target proto-oncogene, over-expression of which
CC is associated with cancer, comprises host cells transfected with a
CC construct containing at least one transgene related to the proto-oncogene
CC and driven by a strong promoter. The product of the transgene induces
CC immunoreactivity to host self-determinants on the product of
CC proto-oncogene. The cellular immunogens are used for protective
CC vaccination against cancer (e.g. carcinoma of breast or colon, or various
CC lymphomas) and for immunotherapy of cancer. Use of the immunogen
CC eliminates the need to isolate immunogenic, HLA host-matched peptides.
CC The method is not based on immune recognition of a determinant defined by
CC a cancer-specific mutation and generates a systemic (anti-metastatic)
CC response.
XX
SQ Sequence 1804 BP; 595 A; 331 C; 428 G; 450 T; 0 other;

Query Match 33.5%; Score 539.8; DB 18; Length 1804;
Best Local Similarity 68.8%; Pred. No. 7.8e-93;
Matches 742; Conservative 0; Mismatches 337; Indels 0; Gaps 0;

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Qy    592 aagggcctcaacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatc 651
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Qy    652 acctcccgcacccagttcaacagcctgcagcagctggtggcctactactccaaacacgcc 711
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Qy    832 cagggctgctttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatc 891
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Qy    892 aaaaccctgaagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatg 951
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Qy   1012 tacatcgtcacggagtacatgagcaaggggagtttgctggacttttctcaaggggagaaca 1071
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Qy   1132 gcgtacgtggagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtg 1191
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Qy   1192 ggagagaacctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaat 1251
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Qy   1252 gagtacacggcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgcc 1311
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Qy   1312 ctctatggccgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgag 1371
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Qy   1372 ctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccag 1431
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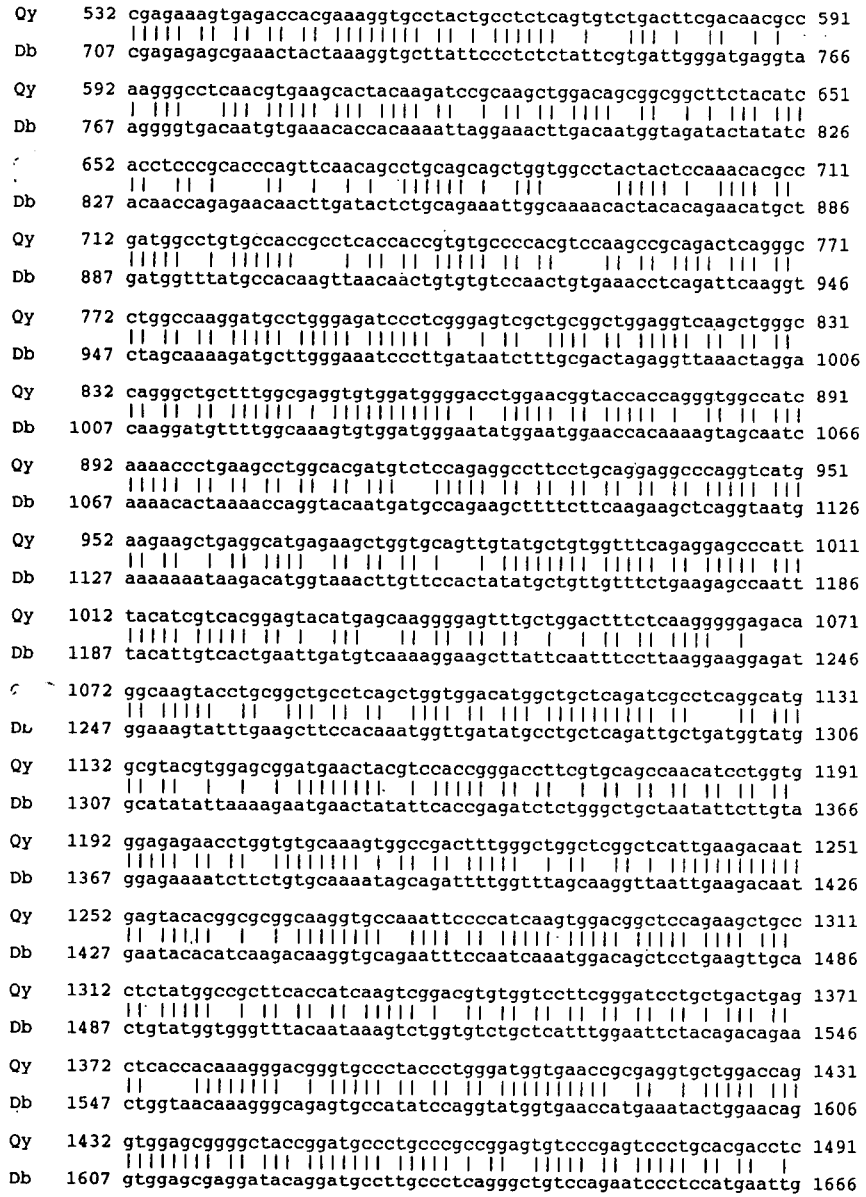
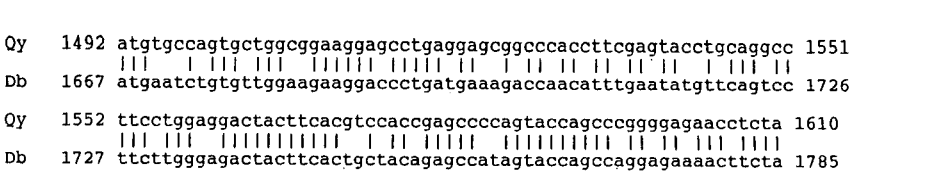
RESULT 14
AAV20462
ID AAV20462 standard; DNA; 1804 BP.
XX
AC AAV20462;
XX
DT 17-JUN-1998 (first entry)
XX
DE Human c-yes oncogene.
XX
KW Human; oncogene; proto-oncogene; neoplastic disease; anticancer;
KW cancer; antisense oligonucleotide; c-yes; ds.
XX
OS Homo sapiens.
XX
PN US5734039-A.
XX
PD 31-MAR-1998.
XX
PF 15-SEP-1994; 94US-0306691.
XX
PR 15-SEP-1994; 94US-0306691.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Calabretta B, Skorski T;
XX
DR WPI; 1998-229882/20.
XX
PT Anticancer composition comprising two anti-sense oligo:nucleotide(s)

CC associated and over expressed proto-oncogenes.
XX
SQ Sequence 1804 BP; 595 A; 331 C; 428 G; 450 T; 0 other;

Query Match 33.5%; Score 539.8; DB 21; Length 1804;
Best Local Similarity 68.8%; Pred. No. 7.8e-93;
Matches 742; Conservative 0; Mismatches 337; Indels 0; Gaps 0;





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Job time: 4213 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 4, 2002, 08:26:28 ; Search time 54.19 Seconds
(without alignments)
7302.373 Million cell updates/sec

Title: US-09-444-711-1
Perfect score: 1611
Sequence: 1 atgggtagcaacaagagcaa.....agcccggggagaacctctag 1611

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1609.4	99.9	1611	1	US-07-820-011A-3	Sequence 3, Appli
2	1609.4	99.9	1611	5	PCT-US93-00445-3	Sequence 3, Appli
3	1216.6	75.5	1602	1	US-07-820-011A-1	Sequence 1, Appli
4	1216.6	75.5	1602	5	PCT-US93-00445-1	Sequence 1, Appli
5	710.2	44.1	4517	5	PCT-US93-06251-83	Sequence 83, Appl
6	689.4	42.8	2647	5	PCT-US93-06251-77	Sequence 77, Appl
7	539.8	33.5	1804	1	US-08-306-691B-40	Sequence 40, Appl
8	539.8	33.5	1804	5	PCT-US93-06251-82	Sequence 82, Appl
9	465.8	28.9	1491	2	US-09-006-675-1	Sequence 1, Appli
10	465.8	28.9	1491	4	US-09-228-603A-1	Sequence 1, Appli
11	346.2	21.5	1574	3	US-09-173-581-12	Sequence 12, Appl
12	346.2	21.5	1574	4	US-09-420-915-12	Sequence 12, Appl
13	341.6	21.2	780	2	US-09-006-675-7	Sequence 7, Appli
14	341.6	21.2	780	4	US-09-228-603A-7	Sequence 7, Appli
15	284	17.6	2770	4	US-08-426-509A-5	Sequence 5, Appli
16	284	17.6	2770	5	PCT-US95-05008-5	Sequence 5, Appli
c 17	284	17.6	7607	1	US-08-222-616-19	Sequence 19, Appl
c 18	284	17.6	7607	5	PCT-US95-04228-19	Sequence 19, Appl
19	252	15.6	271	1	US-08-306-691B-24	Sequence 24, Appl
20	252	15.6	271	5	PCT-US93-06251-66	Sequence 66, Appl
21	249.6	15.5	3623	1	US-08-306-691B-35	Sequence 35, Appl
22	217.6	13.5	728	4	US-09-328-111-821	Sequence 821, App
23	212.4	13.2	1398	2	US-08-604-989A-9	Sequence 9, Appli
24	212.4	13.2	1521	2	US-08-604-989A-10	Sequence 10, Appl
25	212.4	13.2	1942	2	US-08-604-989A-11	Sequence 11, Appl
26	212.4	13.2	2000	4	US-08-426-509A-1	Sequence 1, Appli
27	212.4	13.2	2000	5	PCT-US95-05008-1	Sequence 1, Appli
28	210.8	13.1	255	1	US-08-306-691B-34	Sequence 34, Appl
29	210.8	13.1	255	5	PCT-US93-06251-76	Sequence 76, Appl
30	207.6	12.9	738	2	US-08-604-989A-8	Sequence 8, Appli
31	207.6	12.9	2500	4	US-08-426-509A-3	Sequence 3, Appli
32	207.6	12.9	2500	5	PCT-US95-05008-3	Sequence 3, Appli
33	203.4	12.6	2574	4	US-09-142-529-2	Sequence 2, Appli
34	200	12.4	1987	2	US-08-876-882-1	Sequence 1, Appli
35	182	11.3	194	1	US-08-306-691B-30	Sequence 30, Appl
36	182	11.3	194	5	PCT-US93-06251-72	Sequence 72, Appl
37	181.2	11.2	2505	1	US-08-391-615-1	Sequence 1, Appli
38	170.4	10.6	2674	4	US-09-817-180-1	Sequence 1, Appli
39	165	10.2	3546	1	US-08-162-809-9	Sequence 9, Appli
40	165	10.2	3591	1	US-08-162-809-13	Sequence 13, Appl
41	162.6	10.1	2962	2	US-08-449-645A-10	Sequence 10, Appl
42	162.6	10.1	2962	2	US-08-702-367A-10	Sequence 10, Appl
43	162.6	10.1	2962	5	PCT-US95-04681-10	Sequence 10, Appl
44	161	10.0	4049	1	US-08-162-809-17	Sequence 17, Appl
45	161	10.0	4097	1	US-08-162-809-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-07-820-011A-3
; Sequence 3, Application US/07820011A
; Patent No. 5336615
; GENERAL INFORMATION:
;   APPLICANT: Bell, Leonard
;   APPLICANT: Madri, Joseph A.
;   APPLICANT: Warren, Stephen L.
;   APPLICANT: Luthringer, Daniel J.
;   TITLE OF INVENTION: Genetically Engineered
;   TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
;   TITLE OF INVENTION: Migration
;   TITLE OF INVENTION: and Plasminogen Activator Activity
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Maurice M. Klee
;     STREET: 1951 Burr Street
;     CITY: Fairifield
;     STATE: Connecticut
;     COUNTRY: USA
;     ZIP: 06430
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 5.25 inch, 360 Kb storage
;     COMPUTER: IBM PC XT
;     OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
;     SOFTWARE: Displaywrite 3
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/820,011A
;     FILING DATE: 19920106
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Klee, Maurice M.
;     REGISTRATION NUMBER: 30,399
;     REFERENCE/DOCKET NUMBER: LB-101
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (203) 255 1400
;     TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1611
;     TYPE: NUCLEIC ACID
;     STRANDEDNESS: Double
;     TOPOLOGY: Linear
;   MOLECULE TYPE: cDNA to mRNA
;   HYPOTHETICAL: No
;   ANTI-SENSE: No
;   ORIGINAL SOURCE:
;     ORGANISM: Homo sapien
;   POSITION IN GENOME:
;     CHROMOSOME/SEGMENT: Chromosome 20
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DD 1561 GACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGGAGAACCTCTAG 1611

RESULT 2
PCT-US93-00445-3
; Sequence 3, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820,011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1611
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 20
; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Tanaka, Akio
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: Human Cellular src Gene:
; TITLE: Nucleotide Sequence and Derived Amino
; TITLE: Acid Sequence of the Region Coding for
; TITLE: the Carboxy-Terminal Two-Thirds of
; TITLE: pp60c-src
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; ISSUE: 5
; PAGES: 1122-1129
; DATE: May, 1985
; PUBLICATION INFORMATION:
; AUTHORS: Tanaka, Akio
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Arthur, Richard R.
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: DNA Sequence Encoding the
; TITLE: Amino-Terminal Region of the Human c-src
; TITLE: Protein: Implications of Sequence
; TITLE: Divergence among src-Type Kinase
; TITLE: Oncogenes
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 7
; ISSUE: 5
; PAGES: 1978-1983
; DATE: May, 1987
PCT-US93-00445-3

Query Match 99.9%; Score 1609.4; DB 5; Length 1611;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 ATGGGTAGCAACAAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAGCCTGGAGCCC 60

Qy     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120
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Db     61 GCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCGCCTCGCAGACCCCCAGCAAG 120

Qy    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgcccccgcggccgccgag 180
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Db    121 CCAGCCTCGGCCGACGGCCACCGCGGCCCCAGCGCGGCCTTCGCCCCCGCGGCCGCCGAG 180

Qy    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240
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Db    181 CCCAAGCTGTTCGGAGGCTTCAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGC 240

Qy    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCGCTGGCCGGTGGAGTGACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAG 300

Qy    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagac 360
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Db    301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACACAGAGGGAGAC 360

Qy    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420
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Qy    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480
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Db    421 GCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAG 480

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Db    481 TCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGT 540

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Db    541 GAGACCACGAAAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600

Qy    601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660
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Db    601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGC 660

Qy    661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720
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Db    661 ACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG 720

Qy    721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780
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Db    721 TGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGGCCTGGCCAAG 780

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Qy    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420
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Db    352 TGGTGGCTGGCTCATTCCCTCACTACAGGACAGACGGGCTACATCCCCAGTAACTATGTC 411

Qy    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480
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Db    412 GCGCCCTCAGACTCCATCCAGGCTGAAGAGTGGTACTTTGGGAAGATCACTCGTCGGGAG 471

Qy    481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540
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Db    472 TCCGAGCGGCTGCTGCTCAACCCCGAAAACCCCCGGGGAACCTTCTTGGTCCGGGAGAGC 531

Qy    541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600
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Db    532 GAGACGACAAAAGGTGCCTATTGCCTCTCCGTTTCTGACTTTGACAACGCCAAGGGGCTC 591

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Db    592 AATGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCACGC 651

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Db    652 ACACAGTTCAGCAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACATGCTGATGGCTTG 711

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Db    712 TGCCACCGCCTGACCAACGTCTGCCCCACGTCCAAGCCCCAGACCCAGGGACTCGCCAAG 771

Qy    781 gatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgc 840
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Db    772 GACGCGTGGGAAATCCCCCGGGAGTCGCTGCGGCTGGAGGTGAAGCTGGGGCAGGGCTGC 831

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Db    832 TTTGGAGAGGTCTGGATGGGGACCTGGAACGGCACCACCAGAGTGGCCATAAAGACTCTG 891

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Db    892 AAGCCCGGCAACATGTCCCCGGAGGCCTTCCTGCAGGAAGCCCAAGTGATGAAGAAGCTC 951

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Db    952 CGGCATGAGAAGCTGGTTCAGCTGTACGCAGTGGTGTCGGAAGAGCCCATCTACATCGTC 1011

Qy   1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtac 1080
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Db   1012 ACTGAGTACATGAGCAAGGGGAGCCTCCTGGATTTCCTGAAGGGAGAGATGGGCAAGTAC 1071

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Db   1072 CTGCGGCTGCCACAGCTCGTCGATATGGCTGCTCAGATTGCATCCGGCATGGCCTATGTG 1131

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Db   1132 GAGAGGATGAACTACGTGCACCGAGACCTGCGGGCGGCCAACATCCTGGTGGGGGAGAAC 1191

Qy   1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260
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Db   1192 CTGGTGTGCAAGGTGGCTGACTTTGGGCTGGCACGCCTCATCGAGGACAACGAGTACACA 1251

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Db   1372 AAGGGCCGGGTGCCATACCCAGGGATGGTCAACAGGGAGGTGCTGGACCAGGTGGAGAGG 1431

Qy   1441 ggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccag 1500
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Db   1432 GGCTACCGCATGCCCTGCCCGCCCGAGTGCCCCGAGTCGCTGCATGACCTCATGTGCCAG 1491

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Db   1552 GACTACTTCACCTCGACAGAGCCCCAGTACCAGCCTGGAGAGAACCTATAG 1602
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RESULT 4
PCT-US93-00445-1
; Sequence 1, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820,011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1602 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Gallus, gallus
; PUBLICATION INFORMATION:
; AUTHORS: Takeya, Tatsuo
; AUTHORS: Hanafusa, Hidesaburo
; TITLE: Structure and Sequence of the
; TITLE: Cellular Gene Homologous to the RSV src
; TITLE: Gene and the Mechanism for Generating the
; TITLE: Transforming Virus
; JOURNAL: Cell
; VOLUME: 32
; PAGES: 881-890
; DATE: March, 1983
PCT-US93-00445-1

; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-83

Query Match 44.1%; Score 710.2; DB 5; Length 4517;
Best Local Similarity 70.1%; Pred. No. 2.2e-135;
Matches 955; Conservative 0; Mismatches 408; Indels 0; Gaps 0;

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Qy    308 tgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagactggtggc 367
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Qy    368 tggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtggcgccct 427
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Qy    428 ccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggagtcagagc 487
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Qy    488 ggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagtgagacca 547
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Db    716 GATTACTTTTGAATCCTGGAAATCAACGAGGTATTTTCTTAGTAAGAGAGAGTGAAACAA 775

Qy    548 cgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaacgtga 607
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Db    776 CTAAAGGTGCTTATTCCCTTTCTATTCGTGATTGGGATGAGATAAGGGGTGACAATGTGA 835

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          | |||||||| ||  | || || |||| || || | ||| |||||  || |  | || |
Db    836 AACACTACAAAATTAGGAAACTTGACAATGGTGGATACTATATCACAACCAGAGCACAAT 895

Qy    668 tcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctgtgccacc 727
          |  | |  |||||| |  |||||    ||||| |  |||| || |||||  | ||||||
Db    896 TTGATACTCTGCAGAAATTGGTGAAACACTACACAGAACATGCTGATGGTTTATGCCACA 955

Qy    728 gcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaaggatgcct 787
            | || || ||||| || ||    || || |||||||| || || || |||||| |
Db    956 AGTTGACAACTGTGTGTCCAACTGTGAAACCTCAGACTCAAGGTCTAGCAAAAGATGCTT 1015

Qy    788 gggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgctttggcg 847
          |||| |||||||| || ||  |||| || ||||| || || || || || || || ||||
Db   1016 GGGAAATCCCTCGAGAATCTTTGCGACTAGAGGTTAAACTAGGACAAGGATGTTTCGGCG 1075

Qy    848 aggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaagcctg 907
          | |||||||||| || ||||| || ||||| |  || || |||||||| || || || |
Db   1076 AAGTGTGGATGGGAACATGGAATGGAACCACGAAAGTAGCAATCAAAACACTAAAACCAG 1135

Qy    908 gcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcatg 967
          | || |||   ||||| || ||||| || || || ||| | ||||| ||  | || ||||
Db   1136 GTACAATGATGCCAGAAGCTTTCCTTCAAGAAGCTCAGATAATGAAAAAATTAAGACATG 1195

Qy    968 agaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtcacggagt 1027
          | || || || |   | |||||||| ||||| || || || |||||||| ||||| || |
Db   1196 ATAAACTTGTTCCACTATATGCTGTTGTTTCTGAAGAACCAATTTACATTGTCACTGAAT 1255

Qy   1028 acatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtacctgcggc 1087
            |||   || || || ||  | || || || ||||  |     || |||||  ||  ||
Db   1256 TTATGTCAAAAGGAAGCTTATTAGATTTCCTTAAGGAAGGAGATGGAAAGTATTTGAAGC 1315

Qy   1088 tgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggagcgga 1147
          | || |||||||| || |||||||||||||| ||    || ||||| ||  | ||  | |
Db   1316 TTCCACAGCTGGTTGATATGGCTGCTCAGATTGCTGATGGTATGGCATATATTGAAAGAA 1375

Qy   1148 tgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaacctggtgt 1207
          |||||||  | ||||| || ||||| || || || || || || || ||||| || || ||||
Db   1376 TGAACTATATTCACCGAGATCTTCGGGCTGCTAATATTCTTGTAGGAGAAAATCTTGTGT 1435

Qy   1208 gcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacggcgcggc 1267
          ||||| | || |||||||| | ||  || | ||||||||||||||| ||||| ||  | |
Db   1436 GCAAAATAGCAGACTTTGGTTTAGCAAGGTTAATTGAAGACAATGAATACACAGCAAGAC 1495

Qy   1268 aaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggccgcttca 1327
          ||||||| ||||| || ||||| ||||| ||||| |||||||| || ||||| || || |
Db   1496 AAGGTGCAAAATTTCCAATCAAATGGACAGCTCCTGAAGCTGCACTGTATGGTCGGTTTA 1555

Qy   1328 ccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccacaaagggac 1387
          | || ||||| || || ||||| || || || ||||  || || ||    |||||||| |
Db   1556 CAATAAAGTCTGATGTCTGGTCATTTGGAATTCTGCAAACAGAACTAGTAACAAAGGGCC 1615

Qy   1388 gggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcggggctacc 1447
          | ||||| || || || |||||||||||| || || || || || |||||||| || |||
Db   1616 GAGTGCCATATCCAGGTATGGTGAACCGTGAAGTACTAGAACAAGTGGAGCGAGGATACA 1675

Qy   1448 ggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccagtgctggc 1507
          ||||||| ||||| | ||  ||||| || ||||| || ||  | |||   | ||| |||
Db   1676 GGATGCCGTGCCCTCAGGGCTGTCCAGAATCCCTCCATGAATTGATGAATCTGTGTTGGA 1735

Qy   1508 ggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggaggactact 1567
           |||||| ||||| ||  | || || || || ||  | ||| |||| |||| ||||||||
Db   1736 AGAAGGACCCTGATGAAAGACCAACATTTGAATATATTCAGTCCTTCTTGGAAGACTACT 1795

Qy   1568 tcacgtccaccgagccccagtaccagcccggggagaacctcta 1610
          |||| | || ||||| |||||||||||| || || ||  | ||
Db   1796 TCACTGCTACAGAGCCACAGTACCAGCCAGGAGAAAATTTATA 1838
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RESULT 6
PCT-US93-06251-77
; Sequence 77, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

Query Match 33.5%; Score 539.8; DB 1; Length 1804;
Best Local Similarity 68.8%; Pred. No. 5.7e-101;
Matches 742; Conservative 0; Mismatches 337; Indels 0; Gaps 0;

```
Qy    532 cgagaaagtgagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgcc 591
          ||||| || || || || |||||||| || | ||||||  |   ||| |  ||  | |
Db    707 CGAGAGAGCGAAACTACTAAAGGTGCTTATTCCCTCTCTATTCGTGATTGGGATGAGGTA 766

Qy    592 aagggcctcaacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatc 651
          | |||   ||| ||||| ||| |||| ||  | || || ||||  ||  | | ||| |||
Db    767 AGGGGTGACAATGTGAAACACCACAAAATTAGGAAACTTGACAATGGTAGATACTATATC 826

Qy    652 acctcccgcacccagttcaacagcctgcagcagctggtggcctactactccaaacacgcc 711
          ||  || |    ||  |  | |  |||||| |  |||      ||||| |  |||| ||
Db    827 ACAACCAGAGAACAACTTGATACTCTGCAGAAATTGGCAAAACACTACACAGAACATGCT 886

Qy    712 gatggcctgtgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggc 771
          |||||  | ||||||    | || || ||||| || ||    || || |||| ||| ||
Db    887 GATGGTTTATGCCACAAGTTAACAACTGTGTGTCCAACTGTGAAACCTCAGATTCAAGGT 946

Qy    772 ctggccaaggatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggc 831
          || || || ||||| ||||| |||||| |  | ||  |||| || ||||| || || ||
Db    947 CTAGCAAAAGATGCTTGGGAAATCCCTTGATAATCTTTGCGACTAGAGGTTAAACTAGGA 1006

Qy    832 cagggctgctttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatc 891
          || || || |||||| | |||||||||| |  ||||| || ||||| |  || || |||
Db   1007 CAAGGATGTTTTGGCAAAGTGTGGATGGGAATATGGAATGGAACCACAAAAGTAGCAATC 1066

Qy    892 aaaaccctgaagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatg 951
          ||||| || || || || || |||   ||||| || || || || || || ||||| |||
Db   1067 AAAACACTAAAACCAGGTACAATGATGCCAGAAGCTTTTCTTCAAGAAGCTCAGGTAATG 1126

Qy    952 aagaagctgaggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatt 1011
          || ||  | || ||||  || || || |   | |||||||| ||||| || ||||| |||
Db   1127 AAAAAAATAAGACATGGTAAACTTGTTCCACTATATGCTGTTGTTTCTGAAGAGCCAATT 1186

Qy   1012 tacatcgtcacggagtacatgagcaaggggagtttgctggactttctcaaggggagaca 1071
          ||||| ||||| || |  |||   || || || ||  |  | || || ||||  |
Db   1187 TACATTGTCACTGAATTGATGTCAAAAGGAAGCTTATTCAATTTCCTTAAGGAAGGAGAT 1246

Qy   1072 ggcaagtacctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatg 1131
          || |||||  ||  ||| || ||  |||| || ||| ||||||||| ||    || |||
Db   1247 GGAAAGTATTTGAAGCTTCCACAAATGGTTGATATGCCTGCTCAGATTGCTGATGGTATG 1306

Qy   1132 gcgtacgtggagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtg 1191
          || ||  |  |  | ||||||||  | ||||| || ||  | || || || || || ||
Db   1307 GCATATATTAAAAGAATGAACTATATTCACCGAGATCTCTGGGCTGCTAATATTCTTGTA 1366

Qy   1192 ggagagaacctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaat 1251
          ||||| || ||  |||||||| | || || |||||  | ||  || | ||||||||||||
Db   1367 GGAGAAAATCTTCTGTGCAAAATAGCAGATTTTGGTTTAGCAAGGTTAATTGAAGACAAT 1426

Qy   1252 gagtacacggcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgcc 1311
          || ||||||  |  | |||||||| |||| || ||||| ||||| ||||| |||| |||
Db   1427 GAATACACATCAAGACAAGGTGCAGAATTTCCAATCAAATGGACAGCTCCTGAAGTTGCA 1486

Qy   1312 ctctatggccgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgag 1371
          || |||||  | || || || |||||  |  || || || || || || || | ||| ||
Db   1487 CTGTATGGTGGGTTTACAATAAAGTCTGGTGTCTGCTCATTTGGAATTCTACAGACAGAA 1546

Qy   1372 ctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccag 1431
          ||    |||||||  | ||||| || || || ||||||||||  ||  | |||||  |||
Db   1547 CTGGTAACAAAGGGCAGAGTGCCATATCCAGGTATGGTGAACCATGAAATACTGGAACAG 1606

Qy   1432 gtggagcggggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctc 1491
          |||||||| || ||| ||||||| ||||| | ||  ||||| || ||||| || ||  |
Db   1607 GTGGAGCGAGGATACAGGATGCCTTGCCCTCAGGGCTGTCCAGAATCCCTCCATGAATTG 1666

Qy   1492 atgtgccagtgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggcc 1551
          |||   | ||| |||  |||||| ||||| ||  | || || || || ||  | ||| ||
Db   1667 ATGAATCTGTGTTGGAAGAAGGACCCTGATGAAAGACCAACATTTGAATATGTTCAGTCC 1726

Qy   1552 ttcctggaggactacttcacgtccaccgagccccagtaccagcccggggagaacctcta 1610
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          ||| |||  |||||||||||  | || |||||  |||||||||| || || ||| ||||
Db   1727 TTCTTGGGAGACTACTTCACTGCTACAGAGCCATAGTACCAGCCAGGAGAAAACTTCTA 1785
```

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RESULT   8
PCT-US93-06251-82
; Sequence 82, Application PC/TUS9306251
;  GENERAL INFORMATION:
;    APPLICANT:  Wickstrom, Eric and Rife, Jason P.
;    TITLE OF INVENTION:  Trivalent Synthesis of Oligonucleotides Containing
;    TITLE OF INVENTION:  Stereospecific Alkylphosphonates and Arylphosphonates
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06251
;      FILING DATE:  19930630
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  8586
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  516-742-4343
;      TELEFAX:  516-742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  82:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1804 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US93-06251-82
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Query Match 33.5%; Score 539.8; DB 5; Length 1804;
Best Local Similarity 68.8%; Pred. No. 5.7e-101;
Matches 742; Conservative 0; Mismatches 337; Indels 0; Gaps 0;

```
Qy    532 cgagaaagtgagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgcc 591
          ||||| || || || || |||||||| || | ||||||  |   ||| |  ||  | |
Db    707 CGAGAGAGCGAAACTACTAAAGGTGCTTATTCCCTCTCTATTCGTGATTGGGATGAGGTA 766

Qy    592 aagggcctcaacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatc 651
          | |||   ||| ||||| ||| |||| ||  | || || ||||  ||  | | ||| |||
Db    767 AGGGGTGACAATGTGAAACACCACAAAATTAGGAAACTTGACAATGGTAGATACTATATC 826

Qy    652 acctcccgcacccagttcaacagcctgcagcagctggtggcctactactccaaacacgcc 711
          ||  || |    ||  |  | |  |||||| |  |||      ||||| |  |||| ||
Db    827 ACAACCAGAGAACAACTTGATACTCTGCAGAAATTGGCAAAACACTACACAGAACATGCT 886

Qy    712 gatggcctgtgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggc 771
          |||||  | ||||||    | || || ||||| || ||    || || |||| ||| ||
Db    887 GATGGTTTATGCCACAAGTTAACAACTGTGTGTCCAACTGTGAAACCTCAGATTCAAGGT 946

Qy    772 ctggccaaggatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggc 831
          || || || ||||| ||||| |||||| |  | ||  |||| || ||||| || || ||
Db    947 CTAGCAAAAGATGCTTGGGAAATCCCTTGATAATCTTTGCGACTAGAGGTTAAACTAGGA 1006

Qy    832 cagggctgctttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatc 891
          || || || |||||| | |||||||||| |  ||||| || ||||| |  || || |||
Db   1007 CAAGGATGTTTTGGCAAAGTGTGGATGGGAATATGGAATGGAACCACAAAAGTAGCAATC 1066
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Qy    924 ggccttcctgcaggaggcccaggtcatgaagaagctgaggcatgagaagctggtgcagtt 983
          ||||||||  | |||||  |  | |||||||  ||  ||||||  ||||||||  |||
Db    807 TGCCTTCCTTGAAGAGGCAAATCTGATGAAGAGCTTGCAGCATGACCGGCTGGTGCGGTT 866

Qy    984 gtatgc---tgtggtttcagaggagcccatttacatcgtcacggagtacatgagcaaggg 1040
          | ||||   ||||  |   | ||| || || || ||| | || |||||  |||   |||||
Db    867 GCATGCCGTTGTGACTCAGGGGGAACCAATATATATCATTACTGAGTATATGCAAAAGGG 926

Qy   1041 gagtttgctggactttctcaaggggggagacaggcaagtacctgcggctgcctcagctggt 1100
          ||||||||||| || || ||  | ||   ||| |   |||  |  |||  ||| ||  |
Db    927 CAGTTTGCTGGATTTCCTGAAAAGTGAAGAAGGTAGCGACCAACCTCTGATTCAACTCAT 986

Qy   1101 ggacatggctgctcagatcgcctcaggcatggcgtacgtggagcggatgaactacgtccca 1160
          |||  |  |||| ||||| ||   ||| |||  ||   | ||||  |  ||| ||  | ||
Db    987 TGACTTCTCTGCCCAGATTGCAGAAGGAATGTGGTTTATTGAGCAAAGGAATTATATTCA 1046

Qy   1161 ccgggaccttcgtgcagccaacatcctggtgggagagaacctggtgtgcaaagtggccga 1220
          |||  ||  ||  | |||||  |||  ||||||   |||  |   ||  |||||||| | ||  ||
Db   1047 CCGTGATCTGAGGGCAGCAAACTGCCTGGTATCAGAAACTTTGTTGTGCAAAATAGCAGA 1106

Qy   1221 ctttgggctggctcggctcattgaagacaatgagtacacggcgcggcaaggtgccaaatt 1280
          ||||||||||||  ||  | ||  ||  ||||  |||||  ||  ||  ||  |||||  |||||||
Db   1107 CTTTGGGCTGGCCCGAGTGATAGAGGACAGCGAGTATACTGCCAGGGAAGGTACCAAATT 1166

Qy   1281 ccccatcaagtggacggctccagaagctgccctctatggccgcttcaccatcaagtcgga 1340
          ||||||||||||||  | |  || ||||||   ||||||   ||  ||  |||||||  ||
Db   1167 TCCCATCAAGTGGACATCCCTGGAGGCTGCCAATTATGGCTCTTTTACTATCAAGTCAGA 1226

Qy   1341 cgtgtggtccttcgggatcctgctgactgagctcaccacaaagggacgggtgccctaccc 1400
          ||  |||||  ||  ||  |  ||||  |||||  | |  |||  |  ||  ||   ||  ||  ||
Db   1227 TGTATGGTCATTTGGTGTATTGCTAACTGAAATAATAACATATGGGAGGACTCCATATCC 1286

Qy   1401 tgggatggtgaaccgcgaggtgctggaccaggtggagcggggctaccggatgccctgccc 1460
          ||  |||   |||  |||||  |        | |||||  ||  ||  ||  |||||  ||  ||
Db   1287 AGGTATGTCCAACTCGGAGGTAATTACAGCCCTTGAGCGTGGTTATCGCATGCCGTGTCC 1346

Qy   1461 gccggagtgtcccgagtccctgcacgacctcatgtgccagtgctggcggaaggagcctga 1520
                |||||  |    ||  ||  | |||||  ||||||  |||| | ||||  |||||
Db   1347 CAGCACTTGTCCAAAAGAGCTCTACAGCATCATGCTCCAGTGTTGGCAGCAGGACCCTGA 1406

Qy   1521 ggagcggcccaccttcgagtacctgcaggccttcctggaggactacttcacgtccaccga 1580
          | | ||||| || || ||  | |||  | ||||  |||||||  ||| ||  ||||  ||
Db   1407 GCAACGGCCAACGTTTGAATATTTACAGAGCATCCTAGAGGACTTCTTTACTGCCACTGA 1466

Qy   1581 gccccagtaccagcc 1595
             | |||||||||  |
Db   1467 AACACAGTACCAGGC 1481
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```
RESULT 10
US-09-228-603A-1
; Sequence 1, Application US/09228603A
; Patent No. 6291651
;  GENERAL INFORMATION:
;    APPLICANT:  Hemmati-Brivanlou, Ali
;    APPLICANT:  Weinstein, Daniel C.
;    TITLE OF INVENTION:  A NOVEL SRC-FAMILY KINASE AND METHODS OF
;    TITLE OF INVENTION:  USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/228,603A
;      FILING DATE:  12-JAN-1999
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-217 N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1491
US-09-228-603A-1


  Query Match             28.9%;  Score 465.8;  DB 4;  Length 1491;
  Best Local Similarity   61.6%;  Pred. No. 5.2e-86;
  Matches  822;  Conservative    0;  Mismatches  492;  Indels   21;  Gaps    4;

Qy    264 ctttgtggccctctatgactatgagtctaggacggagacagacctgtccttcaagaaagg 323
          | |  ||||  | ||||||||||||                ||  |||  | ||  | ||||||
Db    165 CCTGCTGGCTTTGTATGACTATGATGGAGTCCACCCTGGGGATCTGACTTTTAGGAAAGG 224

Qy    324 cgagcggctccagattgtcaacaacacggagggagactggtggctggcccactcgctcag 383
          || |  ||||   |  | || ||   |   || || ||||||  ||        |
Db    225 GGACCATCTCC---TGCTAAAGAAAGAGTCAGGGGAGTGGTGGGAAGCATGTCTAATTTC 281

Qy    384 cacaggacagacaggctacatccccagcaactacgtggcgccctccgactccatccaggc 443
          ||| ||  |   |||||   | ||||| ||||| || |||   | | | ||| |  |  |
Db    282 CACTGGTGAAGAAGGCTTTGTTCCCAGTAACTATGTAGCGTATTTCAATTCCCTGGAATC 341

Qy    444 tgaggagtggtattttggcaagatcaccagacgggagtcagagcggttactgctcaatgc 503
          ||| ||||||||  |||       || | | |   |||  | ||  ||   |||||   | |
Db    342 TGAAGAGTGGTACTTTAAAGGCATGAGCCGGAAGGAAGCTGAAAGGCAGCTGCTATCTCC 401

Qy    504 agagaacccgagagggaccttcctcgtgcgagaaagtgagaccacgaaaggtgcctactg 563
          |  ||    || ||| | ||| |  | ||||| |||||||| | |||||||   | ||
Db    402 TGTTAATAAAAGTGGGGCTTTCATGATCCGAGACAGTGAGACAATGAAAGGTTGTTTCTC 461

Qy    564 cctctcagtgtctgacttcgacaacgccaagggcctcaacgtgaagcactacaagatccg 623
          ||||||  |||   ||||             ||   ||  ||||| || ||||| || ||
Db    462 CCTCTCTGTGCGAGACT------------CAGGGGACACTGTGAAACATTACAAAATTCG 509

Qy    624 caagctggacagcggcggcttctacatcacctcccgcacccagttcaacagcctgcagca 683
          ||  ||  ||     || || |||| |||  |  | || | ||  ||         |||  |
Db    510 CACACTCGATGATGGAGGTTTCTTCATTTCTACACGGATCCCTTTTCCTTCTTTGCCAGA 569

Qy    684 gctggtggcctactactccaaacacgccgatggcctgtgccaccgcctcaccaccgtgtg 743
          ||||||   | | ||        | |  |||||| |||| ||  |||| || |     ||
Db    570 GCTGGTACGCCATTATCAAGGTAAAGTGGATGGCTTGTGTCAGTGCCTTACAATACCATG 629

Qy    744 ccccacgtccaagccgcagactcagggcctggccaaggatgcctgggagatccctcggga 803
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Db    630 CCAAACTGTGCGTCCAGAGAAACCATG---GGAAAAGGATGCCTGGGAGATCCCGCGCGA 686

Qy    804 gtcgctgcggctggaggtcaagctgggccagggctgctttggcgaggtgtggatggggac 863
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Qy    864 ctggaacggtaccaccagggtggccatcaaaaccctgaagcctggcacgatgtctccaga 923
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Db    747 GTACAATGGACACACAAAAGTAGCTGTAAAAACAATGAAGCCAGGCAGCATGTCCCCCGG 806

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;  CURRENT APPLICATION NUMBER: US/09/420,915
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/173,581
;  EARLIER FILING DATE: 1998-10-15
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PERL Program
; SEQ ID NO 12
;   LENGTH: 1574
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE: -
;   OTHER INFORMATION: 507669
US-09-420-915-12


  Query Match             21.5%;  Score 346.2;  DB 4;  Length 1574;
  Best Local Similarity   70.1%;  Pred. No. 8.5e-62;
  Matches  465;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy     933 gcaggaggcccaggtcatgaagaagctgaggcatgagaagctggtgcagttgtatgctgt 992
           ||  ||||||  |  |||||||| |||||   ||  ||  |||||| | | | || |||||
Db     464 gcccgaggccaacctcatgaagcagctgcaacaccagcggctggttcggctctacgctgt 523

Qy     993 ggtttcagaggagcccatttacatcgtcacggagtacatgagcaaggggagtttgctgga 1052
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Db     524 ggtcacccaggagcccatctacatcatcactgaatacatggagaatgggagtctagtgga 583

Qy    1053 ctttctcaaggggagacaggcaagtacctgcggctgcctcagctggtggacatggctgc 1112
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Db     584 ttttctcaagacccctcaggcatcaagttgaccatcaacaaactcctggacatggcagc 643

Qy    1113 tcagatcgcctcaggcatggcgtacgtggagcggatgaactacgtccaccgggaccttcg 1172
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Db     644 ccaaattgcagaaggcatggcattcattgaagagcggaattatattcatcgtgaccttcg 703

Qy    1173 tgcagccaacatcctggtgggagagaacctggtgtgcaaagtggccgactttgggctggc 1232
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Db     704 ggctgccaacattctggtgtctgacaccctgagctgcaagattgcagactttggcctagc 763

Qy    1233 tcggctcattgaagacaatgagtacacggcgcggcaaggtgccaaattccccatcaagtg 1292
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Qy    1293 gacggctccagaagctgccctctatggccgcttcaccatcaagtcggacgtgtggtcctt 1352
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Qy    1353 cgggatcctgctgactgagctcaccacaaagggacgggtgccctaccctgggatggtgaa 1412
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Qy    1413 ccgcgaggtgctggaccaggtggagcggggctaccggatgccctgcccgccggagtgtcc 1472
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Db     944 cccggaggtgattcagaacctggagcgaggctaccgcatggtgcgccctgacaactgtcc 1003

Qy    1473 cgagtccctgcacgacctcatgtgccagtgctggcggaaggagcctgaggagcggcccac 1532
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Qy    1533 cttcgagtacctgcaggccttcctggaggactacttcacgtccaccgagccccagtacca 1592
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Qy    1593 gcc 1595
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US-09-006-675-7
; Sequence 7, Application US/09006675
; Patent No. 5952213
;  GENERAL INFORMATION:
;    APPLICANT:  Hemmati-Brivanlou, Ali
;    APPLICANT:  Weinstein, Daniel C.
;    TITLE OF INVENTION:  A NOVEL SRC-FAMILY KINASE AND METHODS OF
;    TITLE OF INVENTION:  USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/006,675
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-217
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  780 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..780
US-09-006-675-7


  Query Match             21.2%;  Score 341.6;  DB 2;  Length 780;
  Best Local Similarity   65.8%;  Pred. No. 6.4e-61;
  Matches  513;  Conservative    0;  Mismatches  264;  Indels    3;  Gaps    1;

Qy     787 tgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgctttggc 846
           |||||||||||| || ||||| |||   ||| ||   |||||  ||     ||    |||||
Db       1 TGGGAGATCCCGCGCGAGTCACTGTCACTGCAGAAGAAGCTTGGAGCTGGACAGTTTGGG 60

Qy     847 gaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaagcct 906
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Db      61 GATGTTTGGTTGGCCATGTACAATGGACACACAAAAGTAGCTGTAAAAACAATGAAGCCA 120

Qy     907 ggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcat 966
           ||||  ||||| || |  |||||||  | |||||  |  | |||||||   ||  ||||
Db     121 GGCAGCATGTCCCCCGGTGCCTTCCTTGAAGAGGCAAATCTGATGAAGAGCTTGCAGCAT 180

Qy     967 gagaagctggtgcagttgtatgc---tgtggtttcagaggagcccatttacatcgtcacg 1023
           ||   |||||||| |||| ||||   ||||  |   | ||| || || || ||| | ||
Db     181 GACCGGCTGGTGCGGTTGCATGCCGTTGTGACTCAGGGGGAACCAATATATATCATTACT 240

Qy    1024 gagtacatgagcaaggggagtttgctggacttttctcaaggggagacaggcaagtacctg 1083
           ||||| |||   |||||||||||| || || ||  | ||   ||| |   |||
Db     241 GAGTATATGCAAAAGGGCAGTTTGCTGGATTTCCTGAAAAGTGAAGAAGGTAGCGACCAA 300

Qy    1084 cggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggag 1143
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Db     301 CCTCTGATTCAACTCATTGACTTCTCTGCCCAGATTGCAGAAGGAATGTGGTTTATTGAG 360

Qy    1144 cggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaacctg 1203
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;      CITY:  New York,
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/426,509A
;      FILING DATE:  21-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/232,545
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-0074-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2770 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
US-08-426-509A-5

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Qy    384 cacaggacagac----------------------aggctacatccccagcaactacgtggc 422
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Db    623 GAAAAGACGAGATGGCTCCAGTCAGCAACTACAAGGCTATATTCCTTCTAACTACGTGGC 682

Qy    423 gccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggagtc 482
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Qy    483 agagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagtga 542
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Qy    543 gaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaa 602
            | |   ||||| |  | ||  || |||||  |  |                | ||
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Qy    603 cgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgcac 662
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Db    908 AATCTTTTCAACACTGAACGAATTTGTGAGCCACTACACCAAGACAAGTGACGGCCTGTG 967

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Qy    771 cctggccaaggatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctggg 830
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Qy    891 caaaaccctgaagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcat 950
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Db   1208 GAAGAACCTAAGACATCCAAAGCTTATCCAGCTTTATGCTGTTTGCACTTTAGAAGATCC 1267

Qy   1008 catttacatcgtcacggagtacatgagcaaggggagtttgctggactttctcaaggggga 1067
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Db   1268 AATTTATATTATTACAGAGTTGATGAGACATGGAAGTCTGCAAGAATATCTCCAAAATGA 1327

Qy   1068 gacaggcaagtacctgcggctgcctcagctggtggacatggctgctcagatcgcctcagg 1127
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Qy   1128 catggcgtacgtggagcggatgaactacgtccaccgggaccttcgtgcagccaacatcct 1187
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Qy   1188 ggtgggagagaacctggtgtgcaaagtggccgactttgggctggctcggctcattgaaga 1247
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Qy   1248 caatga---------gtacacggcgcggcaaggtgccaaattccccatcaagtggacggc 1298
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Qy   1359 cctgctgactgagctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcga 1418
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Job time:  3967 sec
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Date: Jun 4, 2002 10:37 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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-Q=/cgn2_1/USPTO_spool/US09444711/runat_04062002_082655_24981/app_query.fasta_1.1693
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
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-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-MAX_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-FMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-QR=US09444711_@CGN1_1_36 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-444-711-1
Query length: 1611
Database: Issued_Patents_AA:*
Database sequences: 231628
Database length: 24425594
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; Patent No. 5336615
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
; TITLE OF INVENTION: Migration
; TITLE OF INVENTION: and Plasminogen Activator Activity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairifield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC XT
; OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820,011A
; FILING DATE: 19920106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: LB-101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; HYPOTHETICAL: No
; FRAGMENT TYPE: Complete Sequence
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Tanaka, Akio
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: Human Cellular src Gene:
; TITLE: Nucleotide Sequence and Derived Amino
; TITLE: Acid Sequence of the Region Coding for
; TITLE: the Carboxy-Terminal Two-Thirds of
; TITLE: pp60c-src
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; ISSUE: 5
; PAGES: 1122-1129
; DATE: May, 1985
; PUBLICATION INFORMATION:
; AUTHORS: Tanaka, Akio
; AUTHORS: Gibbs, Carol P.

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;  GENERAL INFORMATION:
;     APPLICANT:  Ullrich,, Axel
;     APPLICANT:  Gishizsky,, Mikhail
;     APPLICANT:  Sures,, Irman G.
;     TITLE OF INVENTION:  NOVEL MEGAKARYOCYTIC PROTEIN
;     TITLE OF INVENTION:  TYROSINE KINASES
;     NUMBER OF SEQUENCES:  21
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Pennie & Edmonds
;       STREET:  1155 Avenue of the Americas
;       CITY:  New York,
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/426,509A
;       FILING DATE:  21-APR-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/232,545
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Coruzzi, Laura A
;       REGISTRATION NUMBER:  30,742
;       REFERENCE/DOCKET NUMBER:  7683-0074-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-790-9090
;       TELEFAX:  212-869-9741
;       TELEX:  66141 PENNIE
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;     SEQUENCE CHARACTERISTICS:
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seq_documentation_block:
; Sequence 13, Application PC/TUS9505008
;  GENERAL INFORMATION:
;    APPLICANT:  Sugen, Inc.
;    APPLICANT:  515 Galveston Drive
;    APPLICANT:  Redwood City, California 94063-4720
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     484 etProCysProProGluCysProGluSerLeuHisAspLeuMetCysGln 500

    1501 TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGC 1550
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     501 CysTrpArgLysGluProGluGluArgProThrPheGluTyrLeuGlnAl 517

    1551 CTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGG 1600
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     517 aPheLeuGluAspTyrPheThrSerThrGluProGlnTyrGlnProGlyG 534

    1601 AGAACCTC 1608
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     534 luAsnLeu 536

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seq_documentation_block:
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    tent No. 5336615
;  GENERAL INFORMATION:
;    APPLICANT:  Bell, Leonard
;    APPLICANT:  Madri, Joseph A.
;    APPLICANT:  Warren, Stephen L.
;    APPLICANT:  Luthringer, Daniel J.
;    TITLE OF INVENTION:  Genetically Engineered
;    TITLE OF INVENTION:  Endothelial Cells Exhibiting Enhanced
;    TITLE OF INVENTION:  Migration
;    TITLE OF INVENTION:  and Plasminogen Activator Activity
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairifield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb storage
;      COMPUTER:  IBM PC XT
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 2.10
;      SOFTWARE:  Displaywrite 3
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/820,011A
;      FILING DATE:  19920106
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  LB-101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255 1400
;      TELEFAX:  (203) 254 1101
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  533 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Protein
;    HYPOTHETICAL:  No
;    FRAGMENT TYPE:  Complete Sequence
;    ORIGINAL SOURCE:
;      ORGANISM:  Gallus, gallus
;    PUBLICATION INFORMATION:
;      AUTHORS:  Takeya, Tatsuo
;      AUTHORS:  Hanafusa, Hidesaburo
;      TITLE:  Structure and Sequence of the
;      TITLE:  Cellular Gene Homologous to the RSV src
;      TITLE:  Gene and the Mechanism for Generating the
;      TITLE:  Transforming Virus
;      JOURNAL:  Cell
;      VOLUME:  32
;      PAGES:  881-890
;      DATE:  March, 1983
US-07-820-011A-2


alignment_scores:
            Quality: 2660.50              Length:    536
              Ratio:  5.107                Gaps:      1
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alignment_block:
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       1 MetGlySerSerLysSerLysProLysAspProSerGlnArgArgArgSe 17

      51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCG 100
         ||||||||||   :::::::::|||           |||:::|||||||
      17 rLeuGluProProAspSerThrHis.........HisGlyGlyPheProA 31

     101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACCGCGGCCCC 150
         ||||||||||||||:::|||   |||:::   |||   ||||||   |||
      31 laSerGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47

     151 AGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTT 200
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      48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGlyGlyPh 64

     201 CAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCG 250
         ||||:::|||||||||||||||||||||||||||||||   |||||||
      64 eAsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaLeuAlaG 81

     251 GTGGAGTGACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAG 300
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      81 lyGlyValThrThrPheValAlaLeuTyrAspTyrGluSerArgThrGlu 97

     301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACAC 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      98 ThrAspLeuSerPheLysLysGlyGluArgLeuGlnIleValAsnAsnTh 114

     351 GGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCT 400
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     114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrThrGlyGlnThrGlyT 131
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;    ORIGINAL SOURCE:
;      ORGANISM:  Gallus, gallus
;    PUBLICATION INFORMATION:
;      AUTHORS:  Takeya, Tatsuo
;      AUTHORS:  Hanafusa, Hidesaburo
;      TITLE:  Structure and Sequence of the
;      TITLE:  Cellular Gene Homologous to the RSV src
;      TITLE:  Gene and the Mechanism for Generating the
;      TITLE:  Transforming Virus
;      JOURNAL:  Cell
;      VOLUME:  32
;      PAGES:  881-890
;      DATE:  March, 1983
PCT-US93-00445-2


alignment_scores:
           Quality: 2660.50              Length:    536
             Ratio:  5.107                Gaps:      1
 Percent Similarity:  97.201   Percent Identity: 93.843

alignment_block:
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     48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGlyGlyPh 64

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    114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrThrGlyGlnThrGlyT 131

    401 ACATCCCCAGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAG 450
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    131 yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 147

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    501 TGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGA 550
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    164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThrL 181

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    181 ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 197

    601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 650
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    198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheTyrIl 214

    651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
        ||||||||||||||||||||:::|||||||||||||||||||||||||||
    214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231

    701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
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    264 gGluSerLeuArgLeuGluValLysLeuGlyGlnGlyCysPheGlyGluV 281

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        ||||||||||||||||||||||||||||||||||||||||||||||||||
    281 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 297

    901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCAT 950
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        ||||||||||||||||||||||||||||||||||||||||||||||||||
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   1001 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1050
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    331 luGluProIleTyrIleValThrGluTyrMetSerLysGlySerLeuLeu 347

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        ||||||||||||||||||  ||||||||||||||||||||||||||||||
    348 AspPheLeuLysGlyGluMetGlyLysTyrLeuArgLeuProGlnLeuVa 364

   1101 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 1150
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    364 lAspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValGluArgMetA 381

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        ||||||||||||||||||||||||||||||||||||||||||||||||||
    398 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAs 414

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1121 CCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTCCACCGGGACCTT 1170
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 381 laAspGlyMetAlaTyrIleGluArgMetAsnTyrIleHisArgAspLeu 397

1171 CGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTGCAAAGTGGCCGA 1220
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 398 ArgAlaAlaAsnIleLeuValGlyGluAsnLeuValCysLysIleAlaAs 414

1221 CTTTGGGCTGGCTCGGCTCATTGAAGACAATGAGTACACGGCGCGGCAAG 1270
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1271 GTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGC 1320
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 448 ArgPheThrIleLysSerAspValTrpSerPheGlyIleLeuGlnThrGl 464

1371 GCTCACCACAAAGGGACGGGTGCCCTACCCTGGGATGGTGAACCGCGAGG 1420
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 464 uLeuValThrLysGlyArgValProTyrProGlyMetValAsnArgGluV 481

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1471 CCCGAGTCCCTGCACGACCTCATGTGCCAGTGCTGGCGGAAGGAGCCTGA 1520
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 498 ProGluSerLeuHisGluLeuMetAsnLeuCysTrpLysLysAspProAs 514

1521 GGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGGAGGACTACTTCA 1570
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 514 pGluArgProThrPheGluTyrIleGlnSerPheLeuGluAspTyrPheT 531

1571 CGTCCACCGAGCCCCAGTACCAGCCCGGGGAGAACCTC 1608
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; Sequence 14, Application PC/TUS9505008
;  GENERAL INFORMATION:
;    APPLICANT:  Sugen, Inc.
;    APPLICANT:  515 Galveston Drive
;    APPLICANT:  Redwood City, California 94063-4720
;    APPLICANT:  United States of America
;    APPLICANT:  Wissenschaften E.V.
;    APPLICANT:  Hofgarten Str. 2
;    APPLICANT:  Munchen 80539
;    APPLICANT:  Germany
;    TITLE OF INVENTION:  Novel Megakaryocytic Protein Tyrosine
;    TITLE OF INVENTION:  Kinases
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05008
;      FILING DATE:  24-APR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/232,545
;      FILING DATE:  22-APR-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-074
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)790-9090
;      TELEFAX:  (212)869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  543 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
PCT-US95-05008-14


alignment_scores:
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      48 LysGlyThrAlaValAsnPheSerSerLeuSerMetThrProPheGlyGl 64

     184 .............AAGCTGTTCGGAGGCTTCAACTCCTCGGACACCGTCA 220
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     221 CCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTGACCACCTTTGTG 270
         ::      :::      :::   |||:::||||||||||||   ||||||
      81 alProSerSerTyrProAlaGlyLeuThrGlyGlyValThrIlePheVal 97

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;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  536 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  No. 6326469e
US-08-426-509A-12


alignment_scores:
            Quality: 1949.00              Length:    528
              Ratio:  4.350                Gaps:      4
 Percent Similarity:  84.848   Percent Identity: 71.023

alignment_block:
 US-09-444-711-1 x US-08-426-509A-12   ..

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      93 TTTCCCCGCCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGC.... 138
         |   |||   ||||||          |||::::::   :::|||
      24 aHisProProSerGlnTyrAspProAspProThrGlnLeuSerGlyAlaP 41

     139 .....CACCGCGGCCCCAGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCC 183
              |||                 |||      ||||||::::::|||
      41 heThrHisIleProAspPheAsnAsnPheHisAlaAlaAlaValSerPro 57

     184 AAGCTG...TTCGGAGGCTTCAACTCCTCGGACACCGTCACCTCCCCGCA 230
            :::   |||:::|||   :::                  |||
      58 ProValProPheSerGlyProGlyPheTyrProCysAsnThrLeuGlnAl 74

     231 GAGGGCGGGCCCGCTGGCCGGTGGAGTGACCACCTTTGTGGCCCTCTATG 280
          :::::::::     :::||||||||||||   |||:::||||||||||
      74 aHisSerSerIleThrGlyGlyGlyValThrLeuPheIleAlaLeuTyrA 91

     281 ACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAAAGGCGAGCGG 330
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      91 spTyrGluAlaArgThrGluAspAspLeuSerPheGlnLysGlyGluLys 107

     331 CTCCAGATTGTCAACAACACGGAGGGAGACTGGTGGCTGGCCCACTCGCT 380
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     108 PheHisIleIleAsnAsnThrGluGlyAspTrpTrpGluAlaArgSerLe 124

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seq_documentation_block:
; Sequence 1, Application US/08594447
; Patent No. 5776716
;  GENERAL INFORMATION:
;    APPLICANT:  Ron, Dorit
;    APPLICANT:  Napolitano, Eugene W.
;    APPLICANT:  Voronova, Anna F.
;    TITLE OF INVENTION:  METHODS FOR IDENTIFYING AGENTS WHICH
;    TITLE OF INVENTION:  BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW - Ste. 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/594,447
;      FILING DATE:  31-JAN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22550-20025.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 822-0168
;      TELEX:  90-4030 MRSNFOERSWSH
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  532 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-594-447-1


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            Quality: 1944.00              Length:    550
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; Sequence 11, Application US/08426509A
; Patent No. 6326469
;  GENERAL INFORMATION:
;    APPLICANT:  Ullrich,, Axel
;    APPLICANT:  Gishizsky,, Mikhail
;    APPLICANT:  Sures,, Irman G.
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      ||||||||||||   :::||||||   |||||||||:::||||||   ::
  485 MetProCysProGlnAspCysProIleSerLeuHisGluLeuMetIleHi 501

 1500 GTGCTGGCGGAAGGAGCCTGAGGAGCGGCCCCACCTTCGAGTACCTGCAGG 1549
      :||||||:::|||:::||||||||||||||||||||||||||||||||||:
  501 sCysTrpLysLysAspProGluGluArgProThrPheGluTyrLeuGlnS 518

 1550 CCTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGG 1599
      ::|||||||||||||||||||||:::||||||||||||||||||||||||
  518 erPheLeuGluAspTyrPheThrAlaThrGluProGlnTyrGlnProGly 534

 1600 GAGAACCTC 1608
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  535 GluAsnLeu 537

seq_name: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US95-05008-11

seq_documentation_block:
; Sequence 11, Application PC/TUS9505008
;  GENERAL INFORMATION:
;    APPLICANT:  Sugen, Inc.
;    APPLICANT:  515 Galveston Drive
;    APPLICANT:  Redwood City, California 94063-4720
;    APPLICANT:  United States of America
;    APPLICANT:  Wissenschaften E.V.
;    APPLICANT:  Hofgarten Str. 2
;    APPLICANT:  Munchen 80539
;    APPLICANT:  Germany
;    TITLE OF INVENTION:  Novel Megakaryocytic Protein Tyrosine
;    TITLE OF INVENTION:  Kinases
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05008
;      FILING DATE:  24-APR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/232,545
;      FILING DATE:  22-APR-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-074
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)790-9090
;      TELEFAX:  (212)869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  537 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
PCT-US95-05008-11


alignment_scores:
            Quality: 1932.50              Length:    553
              Ratio:  4.201                Gaps:      6
 Percent Similarity:  83.183   Percent Identity: 67.812

alignment_block:
 US-09-444-711-1 x PCT-US95-05008-11   ..

 Align seg 1/1  to: PCT-US95-05008-11  from: 1  to: 537

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       1 MetGlyCysValGlnCysLysAspLysGluAlaThr......LysLeuTh 15

      51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCG 100
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      15 rGluGluArgAspGlySerLeuAsnGlnSerSerGlyTyrArgTyrGlyT 32

     101 CCTCGCAGACCCCCAGCAAGCCAGCCTCG..................... 129
         :::::   ||||||:::          |||
      32 hrAspProThrProGlnHisTyrProSerPheGlyValThrSerIlePro 48

     130 ..................GCCGACGGCCACCGCGGCCCCAGCGCGGCCTT 161
                            |||   |||   :::|||   :::
      49 AsnTyrAsnAsnPheHisAlaAlaGlyGlyGlnGlyLeuThr........ 62

     162 CGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTTCAACTCCTCGG 211
                               :::|||||||||   |||||||||:
      63 .......................ValPheGlyGlyValAsnSerSerS 71

     212 AC...ACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTG 258
         ::   |||   |||         |||:::|||            ||||||
      71 erHisThrGlyThrLeuArgThrArgGlyGlyThr.........GlyVal 84

     259 ACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAGACAGACCT 308
         |||   ||||||||||||||||||||||:::|||||||||   |||||
      85 ThrLeuPheValAlaLeuTyrAspTyrGluAlaArgThrGluAspAspLe 101

     309 GTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACACGGAGGGAG 358
         |||||||   ||||||||:::::::||||||:::|||:::::::|||||||
     101 uSerPheHisLysGlyGluLysPheGlnIleLeuAsnSerSerGluGlyA 118

     359 ACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCC 408
         ||||||||   |||:::||||||:::||||||:::|||||||||||||||
     118 spTrpTrpGluAlaArgSerLeuThrThrGlyGluThrGlyTyrIlePro 134

     409 AGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTT 458
         ||||||||||||||||   ||||||||||||||||||||||||||||||
     135 SerAsnTyrValAlaProValAspSerIleGlnAlaGluGluTrpTyrPh 151

     459 TGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGA 508
         |||||||:::   |||::::::::::||||||   |||||||:::      |
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Percent Similarity: 83.962 Percent Identity: 67.170

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alignment_block:
US-09-444-711-1 x US-08-426-509A-15  ..

Align seg 1/1  to: US-08-426-509A-15  from: 1  to: 529

     13 AAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAGCCTGGAGCCCGC 62
        |||   :::|||      ::::::::::::      :::||||||
      8 LysLeuGluProValAlaThrAlaLysGluAspAlaGlyLeuGluGlyAs 24

     63 CGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCGCCTCGCAGACCC 112
          :::   :::||||||:::            |||   :::   |||
     24 pPheArgSerTyrGlyAlaAlaAspHisTyrGlyPro...AspProThrL 40

    113 CCAGCAAGCCAGCCTCGGCCGACGGCCACCGCGGCCCCAGCGCGGCCTTC 162
        ::::::||||||||||:::   :::|||           :::   |||
     40 ysAlaArgProAlaSerSerPheAlaHisIleProAsnTyrSerAsnPhe 56

    163 GCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTTCAACTCCTCGGA 212
        :::      |||   :::|||            ||||||   :::|||
     57 SerSerGlnAlaIleAsnPro.............GlyPheLeuAspSerGl 69

    213 CACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTGACCA 262
         |||:::                 |||      :::   |||||||||
     69 yThrIle................ArgGlyValSerGlyIleGlyValThrL 81

    263 CCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCC 312
          |||:::||||||||||||||||||:::|||||||||   |||||||:::
     81 euPheIleAlaLeuTyrAspTyrGluAlaArgThrGluAspAspLeuThr 97

    313 TTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACACGGAGGGAGACTG 362
        |||   |||||||||:::::::::|||:::||||||||||||||||||||
     98 PheThrLysGlyGluLysPheHisIleLeuAsnAsnThrGluGlyAspTr 114

    363 GTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCCAGCA 412
        ||||   |||:::||||||||||:::|||:::||||||   ||||||||||
    114 pTrpGluAlaArgSerLeuSerSerGlyLysThrGlyCysIleProSerA 131

    413 ACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGC 462
        ||||||||||||||   ||||||||||||||||||||||||||||||||||
    131 snTyrValAlaProValAspSerIleGlnAlaGluGluTrpTyrPheGly 147

    463 AAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAACCC 512
        ||||||   |||:::::::::::||||||   |||||||:::      |||||
    148 LysIleGlyArgLysAspAlaGluArgGlnLeuLeuSerProGlyAsnPr 164

    513 GAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGAAAGGTGCCTACT 562
        |:::|||:::|||||||:::|||||||||||||||||||||||||||||||
    164 oGlnGlyAlaPheLeuIleArgGluSerGluThrThrLysGlyAlaTyrS 181

    563 GCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTCAACGTGAAGCAC 612
          |||||||:::   |||:::|||:::::::::|||   :::||||||||||
    181 erLeuSerIleArgAspTrpAspGlnThrArgGlyAspHisValLysHis 197

    613 TACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGCAC 662
        ||||||||||||||||||   ||||||:::|||||||||:::|||::
    198 TyrLysIleArgLysLeuAspMetGlyGlyTyrTyrIleThrThrArgVa 214

    663 CCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCG 712
        :|||||||||||||:::|||:::||||||   :::|||   :::      |
    214 lGlnPheAsnSerValGlnGluLeuValGlnHisTyrMetGluValAsnA 231

    713 ATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCGCAG 762
        ||||||||||||:::   |||   :::   |||         |||||||||
    231 spGlyLeuCysAsnLeuLeuIleAlaProCysThrIleMetLysProGln 247

    763 ACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCG 812
        |||   ||||||||||||||||||||||||   |||:::|||:::
    248 ThrLeuGlyLeuAlaLysAspAlaTrpGluIleSerArgSerSerIleTh 264

    813 GCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGA 862
         ||||||   :::|||||||   ||||||||||||:::|||||||:::||||
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    264 rLeuGluArgArgLeuGlyThrGlyCysPheGlyAspValTrpLeuGlyT 281

    863 CCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTGAAGCCTGGCACG 912
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    281 hrTrpAsnGlySerThrLysValAlaValLysThrLeuLysProGlyThr 297

    913 ATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTGAG 962
        |||||||||:::|||||||||:::|||||||||||||||||   |||||
    298 MetSerProLysAlaPheLeuGluGluAlaGlnValMetLysLeuLeuAr 314

    963 GCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTT 1012
        ||||:::||||||||||||||||||||||||||||||||||||||||||||
    314 gHisAspLysLeuValGlnLeuTyrAlaValValSerGluGluProIleT 331

   1013 ACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTTTCTCAAG 1062
        ||||||||||||||:::|||      ||||||||||||||||||||||||
    331 yrIleValThrGluPheMetCysHisGlySerLeuLeuAspPheLeuLys 347

   1063 GGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGTGGACATGGCTGC 1112
        :::      |||:::   ||||||||||||||||||||||||||||||||||
    348 AsnProGluGlyGlnAspLeuArgLeuProGlnLeuValAspMetAlaAl 364

   1113 TCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTCCACC 1162
        ||||:::|||:::||||||||||||:::|||||||||||||||:::||||
    364 aGlnValAlaGluGlyMetAlaTyrMetGluArgMetAsnTyrIleHisA 381

   1163 GGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTGCAAA 1212
        ||||||||||||||||||||||||||||||||||:::|||:::||||||
    381 rgAspLeuArgAlaAlaAsnIleLeuValGlyGluArgLeuAlaCysLys 397

   1213 GTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAATGAGTACACGGC 1262
        :::||||||||||||||||||||||||||||:::|||:::||||||:::
    398 IleAlaAspPheGlyLeuAlaArgLeuIleLysAspAspGluTyrAsnPr 414

   1263 GCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCC 1312
           ||||||:::||||||||||||||||||||||||||||||||||||||||
    414 oCysGlnGlySerLysProProIleLysTrpThrAlaProGluAlaAlaL 431

   1313 TCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCCTTCGGGATCCTG 1362
        ||:::|||||||||||||||||||||||||||||||||||||||||||||
    431 euPheGlyArgPheThrIleLysSerAspValTrpSerPheGlyIleLeu 447

   1363 CTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCCTGGGATGGTGAA 1412
        ||||||||||||   ||||||||||:::|||||||||||||||   ::
    448 LeuThrGluLeuIleThrLysGlyArgIleProTyrProGlyMetAsnLy 464

   1413 CCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGATGCCCTGCCCGC 1462
        :|||||||||||||:::||||||||||:::|||||||:::||||||||||||
    464 sArgGluValLeuGluGlnValGluGlnGlyTyrHisMetProCysProP 481

   1463 CGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAGTGCTGGCGGAAG 1512
        ||   ||||||   ||||||::::::   |||   |||   ||||||
    481 roGlyCysProAlaSerLeuTyrGluAlaMetGluGlnThrTrpArgLeu 497

   1513 GAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGGAGGA 1562
        :::||||||||||||||||||||||||||||||||:::||||||||||||
    498 AspProGluGluArgProThrPheGluTyrLeuGlnSerPheLeuGluAs 514

   1563 CTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGGAG 1602
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    514 pTyrPheThrSerAlaGluProGlnTyrGlnProGlyAsp 527
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OM of: US-09-444-711-1 to: A_Geneseq_032802:* out_format : pfs

Date: Jun 4, 2002 10:36 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09444711/runat_04062002_082655_24969/app_query.fasta_1.1693
-DB=A_Geneseq_032802 -QFMT=fastan -SUFFIX=n2p.rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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Search information block:
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Query length: 1611
Database: A_Geneseq_032802:*
Database sequences: 747574
Database length: 111073796
Search time (sec): 81.300000

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AC AAR39706;
XX
DT 23-DEC-1993 (first entry)
XX
DE Human pp60 c-src protein.
XX
KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX
OS Homo sapiens.
XX
PN WO9314193-A.
XX
PD 22-JUL-1993.
XX
PF 05-JAN-1993; 93WO-US00445.
XX
PR 06-JAN-1992; 92US-0820011.
XX
PA (UYYA) UNIV YALE.
XX
PI Bell L, Luthringer DJ, Madri JA, Warren SL;
XX
DR WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX
PT Genetically engineered endothelial cells - which exhibit enhanced
PT cell migration, urokinase-type plasminogen activator activity,
PT and reduced mononuclear cell adhesion and fibronectin prodn
XX
PS Disclosure; Page 75-77; 91pp; English.
XX
CC The DNA encoding a portion or (more preferably) the entire pp60
CC c-src polypeptide (Given in AAQ46688) is used to transform endothelial
CC cells. Transformed cells produce increased amounts of pp60 c-src and
CC have improved therapeutic properties. They migrate at faster rates
CC than non-transformed counterparts; have an enhanced ability to
CC inhibit the formation of thrombi and/or dissolve thrombi once they
CC have formed and exhibit reduced mononuclear cell adhesion. They can
CC also be used to improve the success of surgical procedures such as
CC coronary angioplasty, heart bypass surgery, vessel graft and stent
CC implantation.
XX
SQ Sequence 536 AA;

alignment_scores:
Quality: 2834.00 Length: 536
Ratio: 5.287 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-444-711-1 x AAR39706 ..

Align seg 1/1 to: AAR39706 from: 1 to: 536

```
       1 ATGGGTAGCAACAAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAG 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 MetGlySerAsnLysSerLysProLysAspAlaSerGlnArgArgArgSe 17

      51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCG 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      17 rLeuGluProAlaGluAsnValHisGlyAlaGlyGlyGlyAlaPheProA 34
```

XX
PF 28-MAY-1999; 99WO-US11780.
XX
PR 29-MAY-1998; 98US-0087220.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Cheresh DA, Eliceiri B, Schwartzberg PL;
XX
DR WPI; 2000-116335/10.
DR N-PSDB; AAZ29700.
XX
PT Using tyrosine kinase Src for modulating angiogenesis in tissues useful
PT in, e.g. treatment of chronic articular rheumatism -
XX
PS Claim 1; Fig 2; 80pp; English.
XX
CC The present sequence is the wild-type chicken c-Src tyrosine kinase.
CC This Src protein can be used to modulate angiogenesis. When the Src
CC protein is inactivated, angiogenesis is inhibited while, when it is
CC activated, angiogenesis is potentiated. The modified or variant Src can
CC be used to treat inflammatory diseases like, arthritis, rheumatoid
CC arthritis, diabetic retinopathy, restenosis, osteoporosis and cancer
CC associated disorders.
XX
SQ Sequence 533 AA;

alignment_scores:
Quality: 2663.50 Length: 536
Ratio: 5.112 Gaps: 1
Percent Similarity: 97.201 Percent Identity: 94.030

alignment_block:
US-09-444-711-1 x AAY44447 ..

Align seg 1/1 to: AAY44447 from: 1 to: 533

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      1 ATGGGTAGCAACAAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAG 50
        ||||||||||:::|||||||||||||||||||   ||||||||||||||||
      1 MetGlySerSerLysSerLysProLysAspProSerGlnArgArgArgSe 17

     51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCG 100
        ||||||||||   :::::::::|||           |||:::|||||||
     17 rLeuGluProProAspSerThrHis.........HisGlyGlyPheProA 31

    101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACCGCGGCCCC 150
        ||||||||||||||:::|||   |||:::   |||   ||||||   |||
     31 laSerGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47

    151 AGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTT 200
        |||   :::|||:::   :::|||:::||||||||||||||||||||||
     48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGlyGlyPh 64

    201 CAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCG 250
        ||||:::|||||||||||||||||||||||||||||||   |||||||
     64 eAsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaLeuAlaG 81

    251 GTGGAGTGACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     81 lyGlyValThrThrPheValAlaLeuTyrAspTyrGluSerArgThrGlu 97

    301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACAC 350
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     98 ThrAspLeuSerPheLysLysGlyGluArgLeuGlnIleValAsnAsnTh 114

    351 GGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCT 400
        |||||||||||||||||||||||||||||:::|||||||||||||||||
    114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrThrGlyGlnThrGlyT 131

    401 ACATCCCCAGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAG 450
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    131 yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 147

    451 TGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAA 500
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    148 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeuLeuAs 164

    501 TGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGA 550
        |   ||||||||||||||||||||||||||||||||||||||||||||||
    164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThrL 181

    551 AAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    181 ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 197

    601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 650
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheTyrIl 214

    651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
        ||||||||||||||||||:::|||||||||||||||||||||||||||||
    214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231

    701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
        ||||||||||||||||||||||||||||||||||:::|||||||||||||
    231 erLysHisAlaAspGlyLeuCysHisArgLeuThrAsnValCysProThr 247

    751 TCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCG 800
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIleProAr 264

    801 GGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 850
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    264 gGluSerLeuArgLeuGluValLysLeuGlyGlnGlyCysPheGlyGluV 281

    851 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    281 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 297

    901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCAT 950
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    298 LysProGlyThrMetSerProGluAlaPheLeuGlnGluAlaGlnValMe 314

    951 GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1000
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    314 tLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValValSerG 331

   1001 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1050
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    331 luGluProIleTyrIleValThrGluTyrMetSerLysGlySerLeuLeu 347

   1051 GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 1100
        ||||||||||||||||||   ||||||||||||||||||||||||||||
    348 AspPheLeuLysGlyGluMetGlyLysTyrLeuArgLeuProGlnLeuVa 364

   1101 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 1150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    364 lAspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValGluArgMetA 381

   1151 ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    381 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGluAsn 397

   1201 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAA 1250
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    398 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAs 414

   1251 TGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTC 1300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    414 nGluTyrThrAlaArgGlnGlyAlaLysProIleLysTrpThrAlaP 431

   1301 CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 1350
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    431 roGluAlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSer 447
```

```
 601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 650
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheTyrIl 214

 651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
     ||||||||||||||||||:::||||||||||||||||||||||||||||
 214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231

 701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
     ||||||||||||||||||||||||||||||||||:::|||||||||||||
 231 erLysHisAlaAspGlyLeuCysHisArgLeuThrAsnValCysProThr 247

 751 TCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCG 800
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIleProAr 264

 801 GGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 850
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 264 gGluSerLeuArgLeuGluValLysLeuGlyGlnGlyCysPheGlyGluV 281

 851 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 281 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 297

 901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCAT 950
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 298 LysProGlyThrMetSerProGluAlaPheLeuGlnGluAlaGlnValMe 314

 951 GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1000
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 314 tLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValValSerG 331

1001 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1050
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 331 luGluProIleTyrIleValThrGluTyrMetSerLysGlySerLeuLeu 347

1051 GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 1100
     ||||||||||||||||||  ||||||||||||||||||||||||||||||
 348 AspPheLeuLysGlyGluMetGlyLysTyrLeuArgLeuProGlnLeuVa 364

1101 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 1150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 364 lAspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValGluArgMetA 381

1151 ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 381 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGluAsn 397

1201 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAA 1250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 398 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAs 414

1251 TGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTC 1300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 414 nGluTyrThrAlaArgGlnGlyAlaLysProIleLysTrpThrAlaP 431

1301 CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 1350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 431 roGluAlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSer 447

1351 TTCGGGATCCTGCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCC 1400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 448 PheGlyIleLeuLeuThrGluLeuThrThrLysGlyArgValProTyrPr 464

1401 TGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGA 1450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 464 oGlyMetValAsnArgGluValLeuAspGlnValGluArgGlyTyrArgM 481

1451 TGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAG 1500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 481 etProCysProProGluCysProGluSerLeuHisAspLeuMetCysGln 497

1501 TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGC 1550
     ||||||||:::::::||||||||||||||||||||||||||||||||||
  498 CysTrpArgArgAspProGluGluArgProThrPheGluTyrLeuGlnAl 514

1551 CTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGG 1600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  514 aPheLeuGluAspTyrPheThrSerThrGluProGlnTyrGlnProGlyG 531

1601 AGAACCTC 1608
     ||||||||
  531 luAsnLeu 533
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seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:AAY44449

seq_documentation_block:

ID AAY44449 standard; Protein; 533 AA.
XX
AC AAY44449;
XX
DT 22-MAR-2000 (first entry)
XX
DE Mutant chicken c-Src tyrosine kinase, SrcA.
XX
KW Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW chicken; mutant Src; SrcA; point mutation; Y527F; phosphorylation;
KW negative regulation; tyrosine; inflammatory disease; osteoporosis;
KW rheumatoid arthritis; diabetic retinopathy; restenosis; cancer.
XX
OS Gallus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 527
FT /label= Y527F
FT /note= "Wild type Tyr replaced with Phe"
XX
PN WO9961590-A1.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11780.
XX
PR 29-MAY-1998; 98US-0087220.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Cheresh DA, Eliceiri B, Schwartzberg PL;
XX
DR WPI; 2000-116335/10.
XX
PT Using tyrosine kinase Src for modulating angiogenesis in tissues useful
PT in, e.g. treatment of chronic articular rheumatism -
XX
PS Claim 3; Page -; 80pp; English.
XX
CC The present sequence is the mutant chicken c-Src tyrosine kinase,
CC SrcA. This sequence has a point mutation, Y527F, to activate c-Src.
CC This site is involved in negative regulation by the kinase CSK.
CC Phosphorylation of Tyr residue at 527 inactivates the protein. But in
CC the mutated SrcA, the regulatory Tyr is replaced with Phe, thus
CC constitutively activating the protein. This mutant Src protein can be
CC used to modulate angiogenesis. When the Src protein is inactivated,
CC angiogenesis is inhibited while, when it is activated, angiogenesis is
CC potentiated. The mutant or variant Src can be used to treat inflammatory
CC diseases like, arthritis, rheumatoid arthritis, diabetic retinopathy,
CC restenosis, osteoporosis and cancer associated disorders.
CC Note: This sequence is not found in the specification, but derived
CC from the sequence in Fig 2.
XX
SQ Sequence 533 AA;

alignment_scores:

```
AC   AAR39705;
XX
DT   23-DEC-1993  (first entry)
XX
DE   Chicken pp60 c-src protein.
XX
KW   Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX
OS   Gallus gallus.
XX
PN   WO9314193-A.
XX
PD   22-JUL-1993.
XX
PF   05-JAN-1993;   93WO-US00445.
XX
PR   06-JAN-1992;   92US-0820011.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Bell L,  Luthringer DJ,  Madri JA,  Warren SL;
XX
DR   WPI; 1993-243209/30.
DR   P-PSDB; AAR39705.
XX
PT   Genetically engineered endothelial cells - which exhibit enhanced
PT   cell migration, urokinase-type plasminogen activator activity,
PT   and reduced mononuclear cell adhesion and fibronectin prodn
XX
PS   Disclosure; Page 64-66; 91pp; English.
XX
CC   The DNA encoding a portion or (more preferably) the entire pp60
CC   c-src polypeptide (Given in AAQ46687) is used to transform endothelial
CC   cells. Transformed cells produce increased amounts of pp60 c-src and
CC   have improved therapeutic properties. They migrate at faster rates
CC   than non-transformed counterparts; have an enhanced ability to
CC   inhibit the formation of thrombi and/or dissolve thrombi once they
CC   have formed and exhibit reduced mononuclear cell adhesion.  They can
CC   also be used to improve the success of surgical procedures such as
CC   coronary angioplasty, heart bypass surgery, vessel graft and stent
CC   implantation.
XX
SQ   Sequence   533 AA;


 nment_scores:
          Quality: 2658.50              Length:    536
            Ratio:  5.103                 Gaps:      1
 Percent Similarity:  97.201   Percent Identity: 93.843

alignment_block:
 US-09-444-711-1 x AAR39705   ..

 Align seg 1/1  to: AAR39705  from: 1  to: 533

       1 ATGGGTAGCAACAAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAG 50
         |||||||||:::||||||||||||||||||   ||||||||||||||||
       1 MetGlySerSerLysSerLysProLysAspProSerGlnArgArgArgSe 17

      51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGGCGCTTTCCCCG 100
         ||||||||||   ::::::::::|||            |||:::|||||||
      17 rLeuGluProProAspSerThrHis.........HisGlyGlyPheProA 31

     101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACCGCGGCCCC 150
         ||||||||||||||:::|||   |||:::   |||   ||||||   |||
      31 laSerGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47

     151 AGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTT 200
         |||   :::|||:::   :::|||:::||||||||||||||||||||||
      48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGlyGlyPh 64

     201 CAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCG 250
         ||||:::||||||||||||||||||||||||||||||   |||||||

      64 eAsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaLeuAlaG 81

     251 GTGGAGTGACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      81 lyGlyValThrThrPheValAlaLeuTyrAspTyrGluSerArgThrGlu 97

     301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACAC 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      98 ThrAspLeuSerPheLysLysGlyGluArgLeuGlnIleValAsnAsnTh 114

     351 GGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCT 400
         ||||||||||||||||||||||||||||||:::|||||||||||||||||
     114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrThrGlyGlnThrGlyT 131

     401 ACATCCCCAGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAG 450
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     131 yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 147

     451 TGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAA 500
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     148 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeuLeuAs 164

     501 TGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGA 550
         |   ||||||||||||||||||||||||||||||||||||||||||||||
     164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThrL 181

     551 AAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     181 ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 197

     601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 650
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheTyrIl 214

     651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
         ||||||||||||||||||:::||||||||||||||||||||||||||||
     214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231

     701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
         ||||||||||||||||||||||||||||||:::|||||||||||||||||
     231 erLysHisAlaAspGlyLeuCysHisArgLeuThrAsnValCysProThr 247

     751 TCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCG 800
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIleProAr 264

     801 GGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 850
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     264 gGluSerLeuArgLeuGluValLysLeuGlyGlnGlyCysPheGlyGluV 281

     851 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     281 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 297

     901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCAT 950
         |||||||||:::||||||||||||||||||||||||||||||||||||||
     298 LysProGlyAsnMetSerProGluAlaPheLeuGlnGluAlaGlnValMe 314

     951 GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1000
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     314 tLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValValSerG 331

    1001 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1050
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     331 luGluProIleTyrIleValThrGluTyrMetSerLysGlySerLeuLeu 347

    1051 GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 1100
         ||||||||||||||||||   ||||||||||||||||||||||||||||
     348 AspPheLeuLysGlyGluMetGlyLysTyrLeuArgLeuProGlnLeuVa 364

    1101 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 1150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     364 lAspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValGluArgMetA 381
```

```
451 TGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAA 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
148 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeuLeuAs 164

501 TGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGA 550
    |  ||||||||||||||||||||||||||||||||||||||||||||||||
164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThrL 181

551 AAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||
181 ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 197

601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheTyrIl 214

651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
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214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231

701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
    ||||||||||||||||||||||||||||||||||:::||||||||||||
231 erLysHisAlaAspGlyLeuCysHisArgLeuThrAsnValCysProThr 247

751 TCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCG 800
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248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIleProAr 264

801 GGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 850
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264 gGluSerLeuArgLeuGluValLysLeuGlyGlnGlyCysPheGlyGluV 281

851 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900
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281 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleMetThrLeu 297

901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCAT 950
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298 LysProGlyThrMetSerProGluAlaPheLeuGlnGluAlaGlnValMe 314

951 GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1000
    ||||||||||||||||||||||||||||||||||||||||||||||||||
314 tLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValValSerG 331

1001 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1050
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331 luGluProIleTyrIleValThrGluTyrMetSerLysGlySerLeuLeu 347

1051 GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 1100
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348 AspPheLeuLysGlyGluMetGlyLysTyrLeuArgLeuProGlnLeuVa 364

1101 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 1150
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364 lAspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValGluArgMetA 381

1151 ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1200
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381 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGluAsn 397

1201 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAA 1250
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398 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAs 414

1251 TGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTC 1300
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414 nGluTyrThrAlaArgGlnGlyAlaLysProIleLysTrpThrAlaP 431

1301 CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 1350
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1351 TTCGGGATCCTGCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCC 1400
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464 oGlyMetValAsnArgGluValLeuAspGlnValGluArgGlyTyrArgM 481

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481 etProCysProProGluCysProGluSerLeuHisAspLeuMetCysGln 497

1501 TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGC 1550
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498 CysTrpArgArgAspProGluGluArgProThrPheGluTyrLeuGlnAl 514

1551 CTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGG 1600
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514 aPheLeuGluAspTyrPheThrSerThrGluProGlnTyrGlnProGlyG 531

1601 AGAACCTC 1608
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531 luAsnLeu 533
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seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:ABG23778

seq_documentation_block:

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ID   ABG23778 standard; Protein; 565 AA.
XX
AC   ABG23778;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #23769.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS87965.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 54137; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
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     516 ProProGluCysProGluSerLeuHisAspLeuMetCysGlnCysTrpAr 532

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     532 gLysGluProGluGluArgProThrPheGluTyrLeuGlnAlaPheLeuG 549

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AC   ABG10302;
XX
     13-FEB-2002  (first entry)

DE   Novel human diagnostic protein #10293.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS74489.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
P    biodiversity  -
X
PS   Claim 20; SEQ ID No 40661; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence  543 AA;
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alignment_block:
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      92 CTTTCCCCGCCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCAC 141
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     271 GCCCTCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAA 320
         ||||||||||||||||||:::||||||      ||||||||||||||||
      98 AlaLeuTyrAspTyrGluAlaArgThrThrGluAspLeuSerPheLysLy 114

     321 AGGCGAGCGGCTCCAGATTGTCAACAACACGGAGGGAGACTGGTGGCTGG 370
         ||||||||||:::||||||:::|||||||||||||||||||||||||   |
     114 sGlyGluArgPheGlnIleIleAsnAsnThrGluGlyAspTrpTrpGluA 131

     371 CCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCCAGCAACTACGTG 420
         ||:::|||::::::||||||:::::|||||||||||||||||||||||||
     131 laArgSerIleAlaThrGlyLysAsnGlyTyrIleProSerAsnTyrVal 147

     421 GCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCAC 470
         ||||||:::||||||||||||||||||||||||||||||||||||:::
     148 AlaProAlaAspSerIleGlnAlaGluGluTrpTyrPheGlyLysMetGl 164

     471 CAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGA 520
          |||:::::::::|||||||||||||||||      |||   ||||||
     164 yArgLysAspAlaGluArgLeuLeuLeuAsnProGlyAsnGlnArgGlyI 181

     521 CCTTCCTCGTGCGAGAAAGTGAGACCACGAAAGGTGCCTACTGCCTCTCA 570
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     181 lePheLeuValArgGluSerGluThrThrLysGlyAlaTyrSerLeuSer 197

     571 GTGTCTGACTTCGACAACGCCAAGGGCCTCAACGTGAAGCACTACAAGAT 620
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     198 IleArgAspTrpAspGluIleArgGlyAspAsnValLysHisTyrLysIl 214

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     214 eArgLysLeuAspAsnGlyGlyTyrTyrIleThrThrArgAlaGlnPheA 231

     671 ACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG 720
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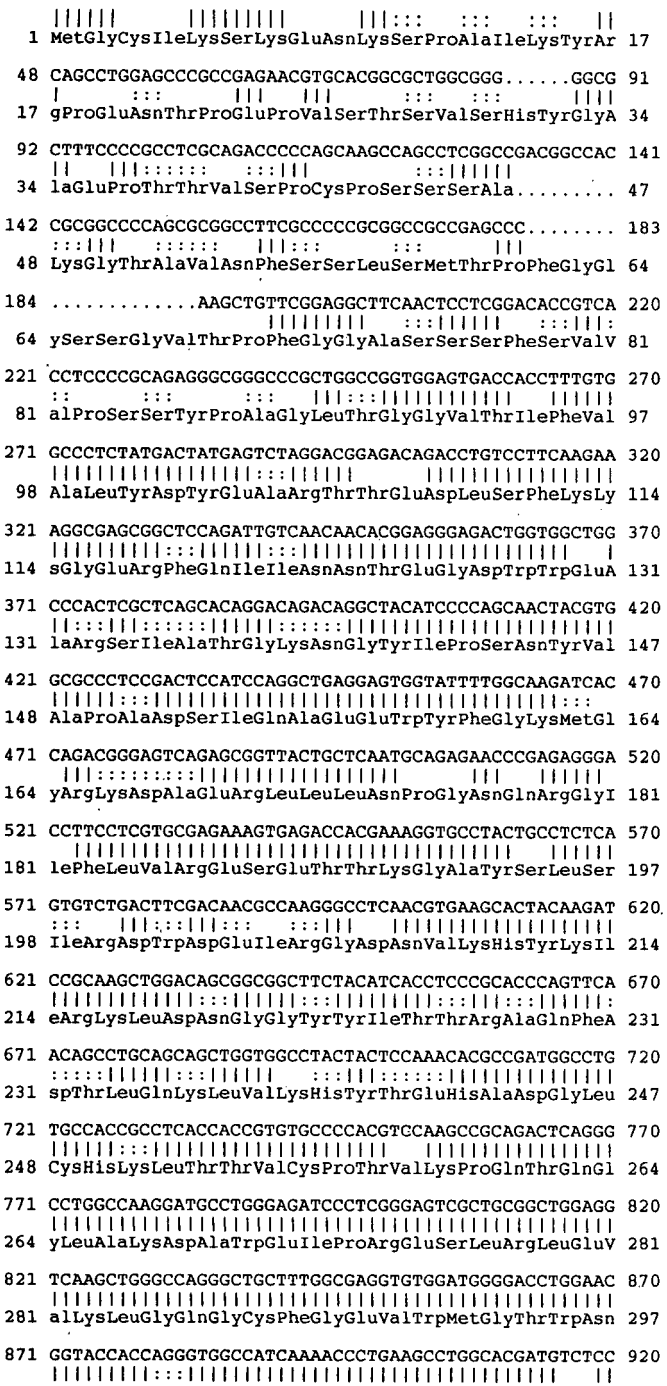

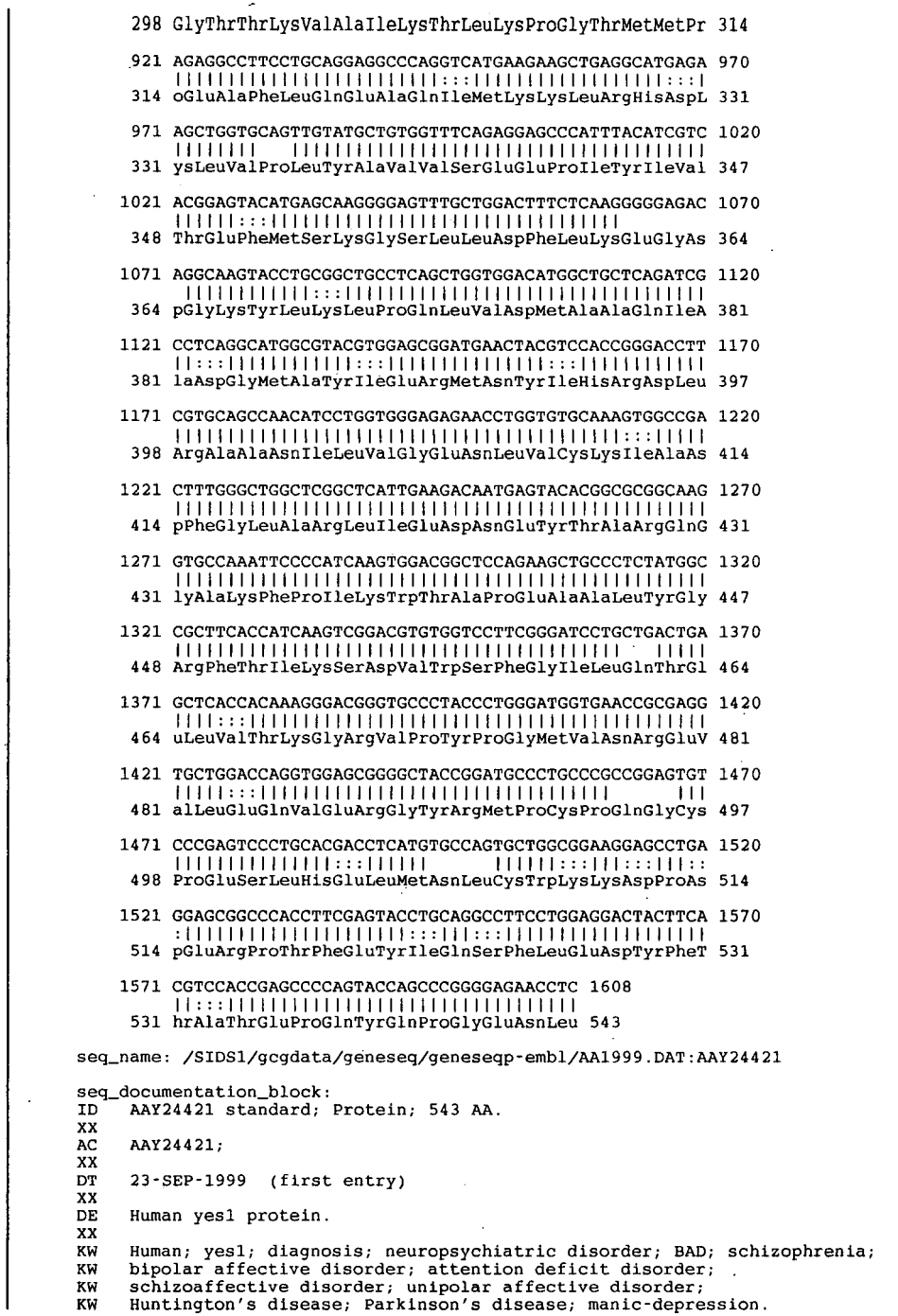

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seq_documentation_block:
ID AAY24421 standard; Protein; 543 AA.
XX
AC AAY24421;
XX
DT 23-SEP-1999 (first entry)
XX
DE Human yes1 protein.
XX
KW Human; yes1; diagnosis; neuropsychiatric disorder; BAD; schizophrenia;
KW bipolar affective disorder; attention deficit disorder;
KW schizoaffective disorder; unipolar affective disorder;
KW Huntington's disease; Parkinson's disease; manic-depression.

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  481 alLeuGluGlnValGluArgGlyTyrArgMetProCysProGlnGlyCys 497

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seq_documentation_block:

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ID   ABG23777 standard; Protein; 351 AA.
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AC   ABG23777;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #23768.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS87964.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 54136; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   351 AA;
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  606 GAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACATCACCT 655
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  756 GCCGCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGT 805
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  806 CGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGG 855
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       |||:::::::||||||:::||||||   :::|||:::|||      ||
 194 ThrPheSerThrLeuGlnGluLeuValAspHisTyrLysLysGlyAsnAs 210

 714 TGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCGCAGA 763
     ||||||||||:::::::|||::::::   |||   :::||||||||||||
 210 pGlyLeuCysGlnLysLeuSerValProCysMetSerSerLysProGln. 226

 764 CTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCGG 813
       :::         ||||||||||||||||||||||||||||||||::::
 227 ..LysProTrpGluLysAspAlaTrpGluIleProArgGluSerLeuLys 242

 814 CTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGAC 863
     ||||||   |||||||||   |||   ||||||||||||||||||:::||
 243 LeuGluLysLysLeuGlyAlaGlyGlnPheGlyGluValTrpMetAlaTh 259

 864 CTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTGAAGCCTGGCACGA 913
     |:::|||      |||:::||||||:::||||||:::|||||||||:::|
 259 rTyrAsnLysHisThrLysValAlaValLysThrMetLysProGlySerM 276

 914 TGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTGAGG 963
     |||||   ||||||||||||   ||||||:::|||||||||   |||:::
 276 etSerValGluAlaPheLeuAlaGluAlaAsnValMetLysThrLeuGln 292

 964 CATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTTA 1013
     |||:::|||||||||:::|||:::|||||||||:::::|||||||||||
 293 HisAspLysLeuValLysLeuHisAlaValValThrLysGluProIleTy 309

1014 CATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTTTCTCAAGG 1063
     ||||:::||||||:::|||:::||||||||||||||||||||||||||:
 309 rIleIleThrGluPheMetAlaLysGlySerLeuLeuAspPheLeuLysS 326

1064 GGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGTGGACATGGCTGCT 1113
     :::::   |||:::         ||||||:::|||:::|||:::::|||
 326 erAspGluGlySerLysGlnProLeuProLysLeuIleAspPheSerAla 342

1114 CAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTCCACCG 1163
     |||||||||:::|||||||||:::::|||:::   ||||||:::||||
 343 GlnIleAlaGluGlyMetAlaPheIleGluGlnArgAsnTyrIleHisAr 359

1164 GGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTGCAAAG 1213
     ||||||||||||||||||||||||:::   :::||||||||||||:
 359 gAspLeuArgAlaAlaAsnIleLeuValSerAlaSerLeuValCysLysI 376

1214 TGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAATGAGTACACGGCG 1263
     ::|||||||||||||||||||::||||||||||||||||||||||||||
 376 leAlaAspPheGlyLeuAlaArgValIleGluAspAsnGluTyrThrAla 392

1264 CGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCT 1313
     |||:::|||||||||||||||||||||||||||||||||||||||||||
 393 ArgGluGlyAlaLysPheProIleLysTrpThrAlaProGluAlaIleAs 409

1314 CTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCCTTCGGGATCCTGC 1363
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 409 nPheGlySerPheThrIleLysSerAspValTrpSerPheGlyIleLeuL 426

1364 TGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCCTGGGATGGTGAAC 1413
     ||   |||::::::|||   |||||||:::|||||||||||||   |||
 426 euMetGluIleValThrTyrGlyArgIleProTyrProGlyMetSerAsn 442

1414 CGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGATGCCCTGCCCGCC 1463
        ||||||:::      :::|||||||||||||||||||||   |||
 443 ProGluValIleArgAlaLeuGluArgGlyTyrArgMetProArgProGl 459

1464 GGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAGTGCTGGCGGAAGG 1513
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 459 uAsnCysProGluGluLeuTyrAsnIleMetMetArgCysTrpLysAsnA 476

1514 AGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGGAGGAC 1563
     ::|||||||||||||||||||||||||||:::|||:::   |||:::|||
 476 rgProGluGluArgProThrPheGluTyrIleGlnSerValLeuAspAsp 492

1564 TACTTCACGTCCACCGAGCCCCAGTACCAG 1593
     :::::::|||:::||||||   |||||||||
 493 PheTyrThrAlaThrGluSerGlnTyrGln 502
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seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:AAB37700

seq_documentation_block:

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ID   AAB37700 standard; protein; 508 AA.
XX
AC   AAB37700;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human lymphocyte kinase.
XX
KW   Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS   Homo sapiens.
XX
PN   WO200070030-A1.
XX
PD   23-NOV-2000.
XX
PF   19-MAY-2000; 2000WO-US13881.
XX
PR   19-MAY-1999;   99US-0134965.
XX
PA   (KINE-) KINETIX PHARM INC.
XX
PI   Zhu X;
XX
DR   WPI; 2000-687708/67.
XX
PT   Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT   comprises a truncated lymphocyte kinase and a ligand, and diffracts
PT   X-rays to determine atomic coordinates at a resolution greater than 5
PT   angstroms -
XX
PS   Claim 1; Page 434-5; 438pp; English.
XX
CC   The present invention relates to a crystal of a protein-ligand complex
CC   comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC   diffracts X-rays so that the atomic coordinates of the protein-ligand
CC   complex can be determined to a resolution of greater than 5.0 Angstroms.
CC   The truncated lck used in the present invention comprises the globular
CC   core of the corresponding full-length lck. The present sequence is the
CC   full-length human lck protein. The crystal of the present invention may
CC   be used to identify kinase inhibitors in screening assays, in drug
CC   screening and drug design processes, to design, select or test inhibitors
CC   of kinase enzymes, where the inhibitors are used as therapeutics for the
```

XX
PN WO9962315-A2.
XX
PD 02-DEC-1999.
XX
PF 27-MAY-1999; 99WO-GB01680.
XX
PR 27-MAY-1998; 98NO-0002419.
PR 30-DEC-1998; 98US-0114240.
XX
PA (LAUR-) LAURAS AS.
PA (JONE/) JONES E L.
XX
PI Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V, Tasken K;
PI Vang T, Altman A, Munshi A;
XX
DR WPI; 2000-086801/07.
DR N-PSDB; AAZ46491.

PT Altering the activity of protein kinase signaling pathways, used for
PT treating immunosuppressive disorders, e.g. AIDS, proliferative
PT disorders, e.g. cancers or autoimmune diseases
XX
PS Claim 23; Page 95-96; 111pp; English.
XX
CC The invention provides a novel method of altering the activity of the
CC protein kinase A (PKA) signaling pathway in a cell that comprises
CC altering the extent of phosphorylation of one or more PKA substrates, or
CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC compositions containing a nucleic acid molecule that encodes a PKA
CC substrate, or fragment, precursor or functionally equivalent variant,
CC where the sequence is modified to alter its susceptibility to
CC phosphorylation by PKA can be used for treating a disorder exhibiting
CC abnormal PKA signaling activity, immunosuppressive disorders or
CC proliferative diseases. They can be used for treating e.g. HIV
CC infection, AIDS, common variable immunodeficiency or cancers. Conditions
CC in which upregulation of the PKA pathway is required, such as autoimmune
CC disease, e.g. systemic lupus erythematosus, may also be treated. The
CC present sequence represents a PKA substrate, wherein the substrate is in
CC the Src-family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk,
CC c-tkl, Fyk, Src-1 or Src-2.
XX
SQ Sequence 509 AA;

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Quality: 1455.00 Length: 454
Ratio: 3.799 Gaps: 3
Percent Similarity: 84.361 Percent Identity: 59.692

alignment_block:
US-09-444-711-1 x AAY49420 ..

Align seg 1/1 to: AAY49420 from: 1 to: 509

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 58 AlaSerProLeuGlnAspAsnLeuVal......IleAlaLeuHisSerTy 72

285 TGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCC 334
    ||||         :::   ||||||:::|||:::|||||||||   |||:
 72 rGluProSerHisAspGlyAspLeuGlyPheGluLysGlyGluProLeuA 89

335 AGATTGTCAACAACACGGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGC 384
    ::|||:::::::::::   |||:::||||||   |||:::|||||||:::
 89 rgIleLeuGluGlnSer...GlyGluTrpTrpLysAlaGlnSerLeuThr 104

385 ACAGGACAGACAGGCTACATCCCCAGCAACTACGTGGCGCCCTCCGACTC 434
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105 ThrGlyGlnGluGlyPheIleProPheAsnPheValAlaLysAlaAsnSe 121

435 CATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAGTCAG 484
    |::::::   |||   |||:::|||   ::::::::::|||::::::::|
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121 rLeuGluProGluProTrpPhePheLysAsnLeuSerArgLysAspAlaG 138

485 AGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGA 534
    |||||   ||||||          |||   :::|||:::||||||:::|||
138 luArgGlnLeuLeuAlaProGlyAsnThrHisGlySerPheLeuIleArg 154

535 GAAAGTGAGACCACGAAAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGA 584
    ||||||||||:::|||   |||::::::   ||||||||   ||||||||
155 GluSerGluSerThrAlaGlySerPheSerLeuSerValArgAspPheAs 171

585 CAACGCCAAGGGCCTCAACGTGAAGCACTACAAGATCCGCAAGCTGGACA 634
    |:::   :::|||      ||||||||||||||||||||:::||||||:
171 pGlnAsnGlnGlyGluValValLysHisTyrLysIleArgAsnLeuAspA 188

635 GCGGCGGCTTCTACATCACCTCCCGCACCCAGTTCAACAGCCTGCAGCAG 684
    ::|||||||||||||||:::   |||      |||   :::|||::::::
188 snGlyGlyPheTyrIleSerProArgIleThrPheProGlyLeuHisGlu 204

685 CTGGTGGCCTACTACTCCAAACACGCCGATGGCCTGTGCCACCGCCTCAC 734
    ||||||   :::|||::::::   :::||||||||||||   ||||||::
205 LeuValArgHisTyrThrAsnAlaSerAspGlyLeuCysThrArgLeuSe 221

735 CACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATG 784
    :      |||   |||:::|||||||||   :::          :::|||
221 rArgProCysGlnThrGlnLysProGln...LysProTrpTrpGluAspG 237

785 CCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAG 834
      ||||||::|||||||||:::|||:::|||      :::|||||||
237 luTrpGluValProArgGluThrLeuLysLeuValGluArgLeuGlyAla 253

835 GGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGAACGGTACCACCAGGGT 884
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254 AlaGlnPheGlyGluValTrpMetGlyTyrTyrAsnGlyHisThrLysVa 270

885 GGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGC 934
    ||||:::|||:::||||||   |||:::|||||||||:::|||||||||
270 lAlaValLysSerLeuLysGlnGlySerMetSerProAspAlaPheLeuA 287

935 AGGAGGCCCAGGTCATGAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTG 984
      ||||||:::::|||||||:::|||:::|||::::::|||||||:::|||
287 laGluAlaAsnLeuMetLysGlnLeuGlnHisGlnArgLeuValArgLeu 303

985 TATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTCACGGAGTACATGAG 1034
    ||||||||||||:::::||||||||||||||||:::||||||||||||::
304 TyrAlaValValThrGlnGluProIleTyrIleIleThrGluTyrMetGl 320

1035 CAAGGGGAGTTTGCTGGACTTTCTCAAGGGGGAGACAGGCAAGTACCTGC 1084
     ::::|||||||||:::||||||||||||      :::|||      |||
320 uAsnGlySerLeuValAspPheLeuLysThrProSerGlyIleLysLeuT 337

1085 GGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCGCCTCAGGCATGGCG 1134
       :::   ::::|||:::||||||||||||||||||||:::||||||||||
337 hrIleAsnLysLeuLeuAspMetAlaAlaGlnIleAlaGluGlyMetAla 353

1135 TACGTGGAGCGGATGAACTACGTCCACCGGGACCTTCGTGCAGCCAACAT 1184
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1185 CCTGGTGGGAGAGAACCTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTC 1234
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1235 GGCTCATTGAAGACAATGAGTACACGGCGCGGCAAGGTGCCAAATTCCCC 1284
     ||||||||||||||||||||||||||||||:::|||||||||||||||
387 rgLeuIleGluAspAsnGluTyrThrAlaArgGluGlyAlaLysPhePro 403

1285 ATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGCCGCTTCACCATCAA 1334
     ||||||||||||||||||||||||      ||||||   ||||||||||
404 IleLysTrpThrAlaProGluAlaIleAsnTyrGlyThrPheThrIleLy 420

1335 GTCGGACGTGTGGTCCTTCGGGATCCTGCTGACTGAGCTCACCACAAAGG 1384
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420 sSerAspValTrpSerPheGlyIleLeuLeuThrGluIleValThrHisG 437
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 160 .........SerGlyAspThrValLysHisTyrLysIleArgThrLeuAs 173

 633 CAGCGGCGGCTTCTACATCACCTCCCGCACCCAGTTCAACAGCCTGCAGC 682
     |:::|||||||||:::|||:::::::|||  .   |||   ||||||   :
 173 pAspGlyGlyPhePheIleSerThrArgIleProPheProSerLeuProG 190

 683 AGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTGTGCCACCGCCTC 732
     ::||||||   :::|||:::      :::||||||||||||:::   |||
 190 luLeuValArgHisTyrGlnGlyLysValAspGlyLeuCysGlnCysLeu 206

 733 ACCACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGGCCTGGCCAAGGA 782
     |||      |||   |||   :::|||:::   :::        |||||
 207 ThrIleProCysGlnThrValArgProGlu...LysProTrpGluLysAs 222

 783 TGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCC 832
     ||||||||||||||||||||||||||||   |||:::   |||||||||
 222 pAlaTrpGluIleProArgGluSerLeuSerLeuGlnLysLysLeuGlyA 239

 833 AGGGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGAACGGTACCACCAGG 882
       |||   ||||||:::||||||:::::   :::||||||   |||:::
 239 laGlyGlnPheGlyAspValTrpLeuAlaMetTyrAsnGlyHisThrLys 255

 883 GTGGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCCAGAGGCCTTCCT 932
     ||||||:::||||||:::|||||||||:::|||||||||   ||||||||
 256 ValAlaValLysThrMetLysProGlySerMetSerProGlyAlaPheLe 272

 933 GCAGGAGGCCCAGGTCATGAAGAAGCTGAGGCATGAGAAGCTGGTGCAGT 982
     |:::||||||:::::|||||||:::|||:::|||:::::|||||||:::|
 272 uGluGluAlaAsnLeuMetLysSerLeuGlnHisAspArgLeuValArgL 289

 983 TGTATGCTGTGGTTTCAGAG...GAGCCCATTTACATCGTCACGGAGTAC 1029
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 289 euHisAlaValValThrGlnGlyGluProIleTyrIleIleThrGluTyr 305

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 306 MetGlnLysGlySerLeuLeuAspPheLeuLysSerGluGluGlySerAs 322

1080 CCTGCGGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCGCCTCAGGCA 1129
           |||   ||||||:::|||:::::::||||||||||||:::||||
 322 pGlnProLeuIleGlnLeuIleAspPheSerAlaGlnIleAlaGluGlyM 339

1130 TGGCGTACGTGGAGCGGATGAACTACGTCCACCGGGACCTTCGTGCAGCC 1179
     ||   ::::::|||:::   ||||||:::|||||||||||||||||||||
 339 etTrpPheIleGluGlnArgAsnTyrIleHisArgAspLeuArgAlaAla 355

1180 AACATCCTGGTGGGAGAGAACCTGGTGTGCAAAGTGGCCGACTTTGGGCT 1229
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 356 AsnCysLeuValSerGluThrLeuLeuCysLysIleAlaAspPheGlyLe 372

1230 GGCTCGGCTCATTGAAGACAATGAGTACACGGCGCGGCAAGGTGCCAAAT 1279
     |||||||:::|||||||||:::|||||||||||||||:::|||:::||||
 372 uAlaArgValIleGluAspSerGluTyrThrAlaArgGluGlyThrLysP 389

1280 TCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGCCGCTTCACC 1329
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1330 ATCAAGTCGGACGTGTGGTCCTTCGGGATCCTGCTGACTGAGCTCACCAC 1379
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 406 IleLysSerAspValTrpSerPheGlyValLeuLeuThrGluIleIleTh 422

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 422 rTyrGlyArgThrProTyrProGlyMetSerAsnSerGluValIleThrA 439

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1480 CTGCACGACCTCATGTGCCAGTGCTGGCGGAAGGAGCCTGAGGAGCGGCC 1529
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 456 LeuTyrSerIleMetLeuGlnCysTrpGlnGlnAspProGluGlnArgPr 472
```

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1530 CACCTTCGAGTACCTGCAGGCCTTCCTGGAGGACTACTTCACGTCCACCG 1579
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 472 oThrPheGluTyrLeuGlnSerIleLeuGluAspPheThrAlaThrG 489

1580 AGCCCCAGTACCAG 1593
     ||   |||||||||
 489 luThrGlnTyrGln 493
```

```
CC   treatment and modulation of diseases, disease symptoms or the effect of
CC   other physiological events mediated by kinases, having one or more kinase
CC   enzymes involved in their pathology.
XX
SQ   Sequence   508 AA;


alignment_scores:
          Quality: 1464.00              Length:    454
            Ratio:  3.812                Gaps:      3
 Percent Similarity:  84.581   Percent Identity: 59.912

alignment_block:
 US-09-444-711-1 x AAB37700   ..

 Align seg 1/1  to: AAB37700  from: 1  to: 508

    235 GCGGGCCCGCTGGCCGGTGGAGTGACCACCTTTGTGGCCCTCTATGACTA 284
        |||:::||||||      :::::::::      :::||||||:::::||
     57 AlaSerProLeuGlnAspAsnLeuVal......IleAlaLeuHisSerTy 71

    285 TGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCC 334
        ||||         :::   ||||||:::|||:::|||||||||:::||:
     71 rGluProSerHisAspGlyAspLeuGlyPheGluLysGlyGluGlnLeuA 88

    335 AGATTGTCAACAACACGGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGC 384
        ::|||:::::::::::::   |||:::||||||   |||:::||||||:::
     88 rgIleLeuGluGlnSer...GlyGluTrpTrpLysAlaGlnSerLeuThr 103

    385 ACAGGACAGACAGGCTACATCCCCAGCAACTACGTGGCGCCCTCCGACTC 434
        |||||||||   |||:::||||||   |||:::||||||   ::::::||
    104 ThrGlyGlnGluGlyPheIleProPheAsnPheValAlaLysAlaAsnSe 120

    435 CATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAGTCAG 484
        |::::::   |||   |||:::|||   :::::::::|||:::::::::|
    120 rLeuGluProGluProTrpPhePheLysAsnLeuSerArgLysAspAlaG 137

    485 AGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGA 534
        |||||   ||||||         |||   :::|||:::||||||:::|||
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    154 GluSerGluSerThrAlaGlySerPheSerLeuSerValArgAspPheAs 170

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        |:::   :::|||      |||||||||||||||||||:::|||||||:
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        ::|||||||||||||||:::   |||      |||   :::|||::::::
    187 snGlyGlyPheTyrIleSerProArgIleThrPheProGlyLeuHisGlu 203

    685 CTGGTGGCCTACTACTCCAAACACGCCGATGGCCTGTGCCACCGCCTCAC 734
        ||||||   :::|||::::::   :::||||||||||||   ||||||::
    204 LeuValArgHisTyrThrAsnAlaSerAspGlyLeuCysThrArgLeuSe 220

    735 CACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATG 784
        :      |||  |||:::||||||||   :::         :::|||
    220 rArgProCysGlnThrGlnLysProGln...LysProTrpTrpGluAspG 236

    785 CCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAG 834
          ||||||:::|||||||||:::|||:::|||      :::||||||
    236 luTrpGluValProArgGluThrLeuLysLeuValGluArgLeuGlyAla 252

    835 GGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGAACGGTACCACCAGGGT 884
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    253 GlyGlnPheGlyGluValTrpMetGlyTyrTyrAsnGlyHisThrLysVa 269

    885 GGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGC 934
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    269 lAlaValLysSerLeuLysGlnGlySerMetSerProAspAlaPheLeuA 286

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    286 laGluAlaAsnLeuMetLysGlnLeuGlnHisGlnArgLeuValArgLeu 302

    985 TATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTCACGGAGTACATGAG 1034
        ||||||||||||:::::::||||||||||||||:::||||||||||||::
    303 TyrAlaValValThrGlnGluProIleTyrIleIleThrGluTyrMetGl 319

   1035 CAAGGGGAGTTTGCTGGACTTTCTCAAGGGGGAGACAGGCAAGTACCTGC 1084
        ::::|||||||||:::||||||||||||      :::|||      |||
    319 uAsnGlySerLeuValAspPheLeuLysThrProSerGlyIleLysLeuT 336

   1085 GGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCGCCTCAGGCATGGCG 1134
          :::   :::|||:::|||||||||||||||||||||||:::|||||||||
    336 hrIleAsnLysLeuLeuAspMetAlaAlaGlnIleAlaGluGlyMetAla 352

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    353 PheIleGluGluArgAsnTyrIleHisArgAspLeuArgAlaAlaAsnIl 369

   1185 CCTGGTGGGAGAGAACCTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTC 1234
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    369 eLeuValSerAspThrLeuSerCysLysIleAlaAspPheGlyLeuAlaA 386

   1235 GGCTCATTGAAGACAATGAGTACACGGCGCGGCAAGGTGCCAAATTCCCC 1284
        ||||||||||||||||||||||||||||||:::||||||||||||||||
    386 rgLeuIleGluAspAsnGluTyrThrAlaArgGluGlyAlaLysPhePro 402

   1285 ATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGCCGCTTCACCATCAA 1334
        ||||||||||||||||||||||||      ||||||   ||||||||||
    403 IleLysTrpThrAlaProGluAlaIleAsnTyrGlyThrPheThrIleLy 419

   1335 GTCGGACGTGTGGTCCTTCGGGATCCTGCTGACTGAGCTCACCACAAAGG 1384
        ||||||||||||||||||||||||||||||||||||:::::::|||   |
    419 sSerAspValTrpSerPheGlyIleLeuLeuThrGluIleValThrHisG 436

   1385 GACGGGTGCCCTACCCTGGGATGGTGAACCGCGAGGTGCTGGACCAGGTG 1434
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    436 lyArgIleProTyrProGlyMetThrAsnProGluValIleGlnAsnLeu 452

   1435 GAGCGGGGCTACCGGATGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCA 1484
        ||||||||||||||||||      |||   :::|||||||||||:::|||::
    453 GluArgGlyTyrArgMetValArgProAspAsnCysProGluGluLeuTy 469

   1485 CGACCTCATGTGCCAGTGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCT 1534
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    469 rGlnLeuMetArgLeuCysTrpLysGluArgProGluAspArgProThrP 486

   1535 TCGAGTACCTGCAGGCCTTCCTGGAGGACTACTTCACGTCCACCGAGCCC 1584
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    486 heAspTyrLeuArgSerValLeuGluAspPhePheThrAlaThrGluGly 502

   1585 CAGTACCAGCCC 1596
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seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:AAY49420

seq_documentation_block:
ID   AAY49420 standard; Protein; 509 AA.
XX
AC   AAY49420;
XX
DT   13-MAR-2000  (first entry)
XX
DE   PKA substrate, Src-family protein.
XX
KW   Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW   kinase substrate; immunosuppressive disorder; proliferative disease;
KW   HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW   systemic lupus erythematosus; Src-family.
XX
OS   Homo sapiens.
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 151 eGlyLysLeuGlyArgLysAspAlaGluArgGlnLeuLeuSerPheGlyA 168

 509 ACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGAAAGGTGCC 558
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 168 snProArgGlyThrPheLeuIleArgGluSerGluThrThrLysGlyAla 184

 559 TACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTCAACGTGAA 608
     |||   ||||||:::   |||:::|||:::   ||||||   :::|||||
 185 TyrSerLeuSerIleArgAspTrpAspAspMetLysGlyAspHisValLy 201

 609 GCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCCC 658
     ||||||||||||||||||||||||:::||||||:::||||||||:::|
 201 sHisTyrLysIleArgLysLeuAspAsnGlyGlyTyrTyrIleThrThrA 218

 659 GCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACAC 708
     ||:::||||||:::::||||||||||||||||   :::||||||:::::
 218 rgAlaGlnPheGluThrLeuGlnGlnLeuValGlnHisTyrSerGluArg 234

 709 GCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCC 758
     |||   |||||||||   ||||||:::::   |||      :::   ||
 235 AlaAlaGlyLeuCysCysArgLeuValValProCysHisLysGlyMetPr 251

 759 GCAGACTCAGGGCCTGGCC.........AAGGATGCCTGGGAGATCCCTC 799
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 800 GGGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAG 849
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 268 rgGluSerLeuGlnLeuIleLysArgLeuGlyAsnGlyGlnPheGlyGlu 284

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 351 uAspPheLeuLysAspGlyGluGlyArgAlaLeuLysLeuProAsnLeuV 368

1100 TGGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATG 1149
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 368 alAspMetAlaAlaGlnValAlaAlaGlyMetAlaTyrIleGluArgMet 384

1150 AACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAA 1199
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 401 yLeuIleCysLysIleAlaAspPheGlyLeuAlaArgLeuIleGluAspA 418

1250 ATGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCT 1299
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 418 snGluTyrThrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAla 434

1300 CCAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTC 1349
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 435 ProGluAlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSe 451

1350 CTTCGGGATCCTGCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACC 1399
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 451 rPheGlyIleLeuLeuThrGluLeuValThrLysGlyArgValProTyrP 468

1400 CTGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGG 1449
     ||||||||   ||||||||||||||:::|||||||||||||||||||||
 468 roGlyMetAsnAsnArgGluValLeuGluGlnValGluArgGlyTyrArg 484

1450 ATGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCA 1499
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; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Ullrich,, Axel
; APPLICANT: Gishizsky,, Mikhail
; APPLICANT: Sures,, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; TITLE OF INVENTION: TYROSINE KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York,
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,509A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/232,545
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-0074-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: No. 6326469e
US-08-426-509A-15

alignment_scores:
Quality: 1856.00 Length: 530
Ratio: 4.171 Gaps: 3

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151 AGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTT 200
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351 GGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCT 400
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117 rGluGlyAspTrpTrpLeuAlaHisSerLeuSerThrGlyGlnThrGlyT 134

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651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
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217 eThrSerArgThrGlnPheAsnSerLeuGlnGlnLeuValAlaTyrTyrS 234

701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
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951 GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1000
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1601 AGAACCTC 1608
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AC   AAY44447;
XX
DT   22-MAR-2000  (first entry)
XX
DE   Wild-type chicken c-Src tyrosine kinase.
XX
KW   Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW   chicken; viral expression vector; replication competent; variant Src;
KW   inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
KW   diabetic retinopathy; osteoporosis; cancer.
XX
OS   Gallus sp.
XX
PN   WO9961590-A1.
XX
PD   02-DEC-1999.
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XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of chicken tyrosine kinase protein Src.
XX
KW Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KW myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KW diabetic retinopathy; inflammatory disease; infection; arthritis;
KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW diabetic retinopathy; psoriasis; neovascular glaucoma;
KW capillary proliferation; osteoporosis; cancer.
XX
OS Gallus sp.
XX
PN WO200145751-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35396.
XX
PR 22-DEC-1999; 99US-0470881.
29-MAR-2000; 2000US-0538248.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Cheresh DA, Eliceiri B, Paul R;
XX
DR WPI; 2001-417982/44.
DR N-PSDB; AAH28357.
XX
PT Modulating vascular permeability in tissues, including inflamed tissue,
PT tissues associated with stroke, myocardial infarction, by contacting
PT the tissue with tyrosine kinase protein Src, Yes or their modified
PT forms -
XX
PS Disclosure; Fig 2; 133pp; English.
XX
CC The specification describes a method for modulating vascular
CC permeability in a tissue suffering from a disease condition. The method
CC comprises contacting the tissue with a pharmaceutical composition
CC comprising tyrosine kinase protein Src, Yes or their mixtures or
CC nucleic acid expressing them. The method is useful for modulating
CC vascular permeability in tissues, including inflamed tissue, tissues
CC associated with stroke, myocardial infarction or other blockage of
CC normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
CC and similar tissues. Pathologies which may be treated include include
CC trauma to blood vessels, and other systemic pathological events such as
CC atherosclerosis, diabetic retinopathy, inflammatory disease due to
CC infection by microbial agents and arthritis. Other diseases which can
CC be treated include adult respiratory distress syndrome (ARDS), rheumatoid
CC arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
CC capillary proliferation in atherosclerotic plaques and osteoporosis and
CC cancer associated disorders such as solid tumours, solid tumour
CC metastases, angiofibromas and hemangiomas. The present sequence
CC represents chicken Src, and is used in the method of the invention.
XX
SQ Sequence 533 AA;

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             Ratio:  5.112              Gaps:      1
 Percent Similarity:  97.201   Percent Identity: 94.030
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alignment_block:

US-09-444-711-1 x AAB84661 ..

Align seg 1/1 to: AAB84661 from: 1 to: 533

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  98 ThrAspLeuSerPheLysLysGlyGluArgLeuGlnIleValAsnAsnTh 114

 351 GGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCT 400
     ||||||||||||||||||||||||||||||:::|||||||||||||||||
 114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrThrGlyGlnThrGlyT 131

 401 ACATCCCCAGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAG 450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 131 yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 147

 451 TGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAA 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 148 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeuLeuAs 164

 501 TGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGA 550
     |   ||||||||||||||||||||||||||||||||||||||||||||||
 164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThrL 181

 551 AAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 181 ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 197
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          Quality: 2659.50              Length:    536
            Ratio:  5.105                Gaps:      1
Percent Similarity:  97.201   Percent Identity: 93.843

alignment_block:
US-09-444-711-1 x AAY44449   ..

Align seg 1/1  to: AAY44449  from: 1  to: 533

      1 ATGGGTAGCAACAAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAG 50
        ||||||||||:::||||||||||||||||||   ||||||||||||||||
      1 MetGlySerSerLysSerLysProLysAspProSerGlnArgArgArgSe 17

     51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCG 100
        ||||||||||   :::::::::|||            |||:::|||||||
     17 rLeuGluProProAspSerThrHis.........HisGlyGlyPheProA 31

    101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACCGCGGCCCC 150
        ||||||||||||||:::|||  |||:::. |||  ||||||  |||
     31 laSerGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47

    151 AGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTT 200
        |||  :::|||:::  :::|||:::||||||||||||||||||||||||
     48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGlyGlyPh 64

    201 CAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCG 250
        ||||:::|||||||||||||||||||||||||||||||   |||||||
     64 eAsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaLeuAlaG 81

    251 GTGGAGTGACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     81 lyGlyValThrThrPheValAlaLeuTyrAspTyrGluSerArgThrGlu 97

    301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACAC 350
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     98 ThrAspLeuSerPheLysLysGlyGluArgLeuGlnIleValAsnAsnTh 114

    351 GGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCT 400
        ||||||||||||||||||||||||||||||:::||||||||||||||||
    114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrThrGlyGlnThrGlyT 131

    401 ACATCCCCAGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAG 450
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    131 yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 147

    451 TGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAA 500
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    148 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeuLeuAs 164

    501 TGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGA 550
        |   ||||||||||||||||||||||||||||||||||||||||||||||
    164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThrL 181

    551 AAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    181 ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 197

    601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 650
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheTyrIl 214

    651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
        ||||||||||||||||||:::||||||||||||||||||||||||||||
    214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231

    701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
        ||||||||||||||||||||||||||||||||:::||||||||||||||
    231 erLysHisAlaAspGlyLeuCysHisArgLeuThrAsnValCysProThr 247

    751 TCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCG 800
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIleProAr 264

    801 GGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 850
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    264 gGluSerLeuArgLeuGluValLysLeuGlyGlnGlyCysPheGlyGluV 281

    851 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    281 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 297

    901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCAT 950
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    298 LysProGlyThrMetSerProGluAlaPheLeuGlnGluAlaGlnValMe 314

    951 GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1000
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    314 tLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValValSerG 331

   1001 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1050
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    331 luGluProIleTyrIleValThrGluTyrMetSerLysGlySerLeuLeu 347

   1051 GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 1100
        ||||||||||||||||||   ||||||||||||||||||||||||||||
    348 AspPheLeuLysGlyGluMetGlyLysTyrLeuArgLeuProGlnLeuVa 364

   1101 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 1150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    364 lAspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValGluArgMetA 381

   1151 ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    381 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGluAsn 397

   1201 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAA 1250
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    398 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAs 414

   1251 TGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTC 1300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    414 nGluTyrThrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAlaP 431

   1301 CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 1350
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    431 roGluAlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSer 447

   1351 TTCGGGATCCTGCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCC 1400
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    448 PheGlyIleLeuLeuThrGluLeuThrThrLysGlyArgValProTyrPr 464

   1401 TGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGA 1450
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    464 oGlyMetValAsnArgGluValLeuAspGlnValGluArgGlyTyrArgM 481

   1451 TGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAG 1500
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    481 etProCysProProGluCysProGluSerLeuHisAspLeuMetCysGln 497

   1501 TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGC 1550
        ||||||||:::::::||||||||||||||||||||||||||||||||||
    498 CysTrpArgArgAspProGluGluArgProThrPheGluTyrLeuGlnAl 514

   1551 CTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGG 1600
        ||||||||||||||||||||||||||||||||||:::||||||||||||
    514 aPheLeuGluAspTyrPheThrSerThrGluProGlnPheGlnProGlyG 531

   1601 AGAACCTC 1608
        ||||||||
    531 luAsnLeu 533

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:AAR39705

seq_documentation_block:
ID   AAR39705 standard; Protein; 533 AA.
XX
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1151 ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 381 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGluAsn 397

1201 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAA 1250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 398 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAs 414

1251 TGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTC 1300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 414 nGluTyrThrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAlaP 431

1301 CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 1350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 431 roGluAlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSer 447

1351 TTCGGGATCCTGCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCC 1400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 448 PheGlyIleLeuLeuThrGluLeuThrThrLysGlyArgValProTyrPr 464

1401 TGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGA 1450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 464 oGlyMetValAsnArgGluValLeuAspGlnValGluArgGlyTyrArgM 481

1451 TGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAG 1500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 481 etProCysProProGluCysProGluSerLeuHisAspLeuMetCysGln 497

1501 TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGC 1550
     |||||||||:::::|||||||||||||||||||||||||||||||||||
 498 CysTrpArgArgAspProGluGluArgProThrPheGluTyrLeuGlnAl 514

1551 CTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGG 1600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 514 aPheLeuGluAspTyrPheThrSerThrGluProGlnTyrGlnProGlyG 531

1601 AGAACCTC 1608
     ||||||||
 531 luAsnLeu 533
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:AAY44451

seq_documentation_block:

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ID   AAY44451 standard; Protein; 533 AA.
XX
AC   AAY44451;
XX
DT   22-MAR-2000  (first entry)
XX
DE   Mutant chicken c-Src tyrosine kinase, Src(K295M).
XX
KW   Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW   chicken; mutant; Src(K295M); point mutation; tumour cell signalling;
KW   ATP binding; proliferation; kinase domain; inflammatory disease; cancer;
KW   osteoporosis; rheumatoid arthritis; diabetic retinopathy; restenosis.
XX
OS   Gallus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 295
FT                   /label= K295M
FT                   /note= "Wild type Lys replaced with Met"
XX
PN   WO9961590-A1.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US11780.
XX
PR   29-MAY-1998;   98US-0087220.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Cheresh DA,  Eliceiri B,  Schwartzberg PL;
XX
DR   WPI; 2000-116335/10.
XX
PT   Using tyrosine kinase Src for modulating angiogenesis in tissues useful
PT   in, e.g. treatment of chronic articular rheumatism -
XX
PS   Claim 6; Page -; 80pp; English.
XX
CC   The present sequence is the mutant chicken c-Src tyrosine kinase,
CC   Src(K295M). This sequence has a point mutation, K295M, in the kinase
CC   domain, which prevents ATP binding and also blocks kinase dependent
CC   Src functions related to vascular cell and tumour cell signalling and
CC   proliferation. This mutant Src(K295M) protein, can be used to modulate
CC   specifically, inhibit angiogenesis. When the Src protein is inactivated,
CC   angiogenesis is inhibited while, when it is activated, angiogenesis is
CC   potentiated. The mutant or variant Src can be used to treat inflammatory
CC   diseases like, arthritis, rheumatoid arthritis, diabetic retinopathy,
CC   restenosis, osteoporosis and cancer associated disorders.
CC   Note: This sequence is not found in the specification, but derived
CC   from the sequence in Fig 2.
XX
SQ   Sequence   533 AA;
```

alignment_scores:

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           Quality: 2657.50            Length:    536
             Ratio:  5.111               Gaps:      1
 Percent Similarity:  97.015   Percent Identity: 93.843
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alignment_block:

US-09-444-711-1 x AAY44451 ..

Align seg 1/1 to: AAY44451 from: 1 to: 533

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   1 ATGGGTAGCAACAAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAG 50
     |||||||||:::|||||||||||||||||||   ||||||||||||||||
   1 MetGlySerSerLysSerLysProLysAspProSerGlnArgArgArgSe 17

  51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCG 100
     |||||||||   :::::::::|||            |||:::|||||||
  17 rLeuGluProProAspSerThrHis.........HisGlyGlyPheProA 31

 101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACCGCGGCCCC 150
     ||||||||||||||:::|||   |||:::   |||   ||||||   |||
  31 laSerGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47

 151 AGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTT 200
     |||   :::|||:::   :::|||:::|||||||||||||||||||||||
  48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGlyGlyPh 64

 201 CAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCG 250
     ||||:::|||||||||||||||||||||||||||||||   |||||||
  64 eAsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaLeuAlaG 81

 251 GTGGAGTGACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAG 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  81 lyGlyValThrThrPheValAlaLeuTyrAspTyrGluSerArgThrGlu 97

 301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACAC 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  98 ThrAspLeuSerPheLysLysGlyGluArgLeuGlnIleValAsnAsnTh 114

 351 GGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCT 400
     ||||||||||||||||||||||||||||||:::|||||||||||||||||
 114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrThrGlyGlnThrGlyT 131

 401 ACATCCCCAGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAG 450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 131 yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 147
```

```
 956 AGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAG 1005
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 134 ysLeuArgHisGluLysLeuValGlnLeuTyrAlaValValSerGluGlu 150

1006 CCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTT 1055
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 151 ProIleTyrIleValThrGluTyrMetSerLysGlySerLeuLeuAspPh 167

1056 TCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGTGGACA 1105
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 167 eLeuLysGlyGluThrGlyLysTyrLeuArgLeuProGlnLeuValAspM 184

1106 TGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGAACTAC 1155
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 184 etAlaAlaGlnIleAlaSerGlyMetAlaTyrValGluArgMetAsnTyr 200

1156 GTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGT 1205
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 201 ValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGluAsnLeuVa 217

1206 GTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAATGAGT 1255
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 217 lCysLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAsnGluT 234

1256 ACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAA 1305
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 234 yrThrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAlaProGlu 250

1306 GCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCCTTCGG 1355
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 251 AlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSerPheGl 267

1356 GATCCTGCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCCTGGGA 1405
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 267 yIleLeuLeuThrGluLeuThrThrLysGlyArgValProTyrProGlyM 284

1406 TGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGATGCCC 1455
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 284 etValAsnArgGluValLeuAspGlnValGluArgGlyTyrArgMetPro 300

1456 TGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAGTGCTG 1505
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 301 CysProProGluCysProGluSerLeuHisAspLeuMetCysGlnCysTr 317

1506 GCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCC 1555
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 317 pArgLysGluProGluGluArgProThrPheGluTyrLeuGlnAlaPheL 334

1556 TGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGGAGAAC 1605
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 334 euGluAspTyrPheThrSerThrGluProGlnTyrGlnProGlyGluAsn 350

1606 CTC 1608
     |||
 351 Leu 351
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seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:AAB99332

seq_documentation_block:

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ID   AAB99332 standard; Protein; 505 AA.
XX
AC   AAB99332;
XX
DT   23-AUG-2001  (first entry)
XX
DE   Human tyrosine kinase Hck protein sequence SEQ ID NO:11.
XX
KW   Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
KW   tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
KW   Hck signal transduction; human immunodeficiency virus; HIV infection;
KW   anticancer.
XX
OS   Homo sapiens.
XX
PN   WO200132869-A1.
XX
PD   10-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-JP07500.
XX
PR   29-OCT-1999;   99JP-0309957.
XX
PA   (SSSE ) SSP CO LTD.
XX
PI   Taniyama T,  Narita T;
XX
DR   WPI; 2001-316440/33.
XX
PT   New proteins which bind to human tyrosine kinase Hck for promotion of
PT   apoptosis and for the elucidation of the mechanism of Hck signal
PT   transduction  -
XX
PS   Example 1; Page 33-35; 45pp; Japanese.
XX
CC   The present invention describes a protein, designated HSB-1, which binds
CC   to human tyrosine kinase Hck. Also described are: (1) nucleic acids
CC   encoding the protein and its derivatives; (2) recombinant vectors
CC   containing the nucleic acids; and (3) host cells transformed by the
CC   vectors and expressing the protein. HSB-1 has cytostatic activity, binds
CC   tyrosine kinase, enhances tumour necrosis factor alpha and promotes
CC   apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
CC   of Hck signal transduction and of the role of Hck in human
CC   immunodeficiency virus (HIV) infection. They can be used for the
CC   treatment of infections and other diseases with which Hck is associated.
CC   They promote the anticancer activity of tumour necrosis factor alpha.
CC   The present sequence represents the human tyrosine kinase Hck protein,
CC   which is used in an example from the present invention.
XX
SQ   Sequence   505 AA;
```

alignment_scores:

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            Quality: 1526.00              Length:    511
              Ratio:  3.731                Gaps:      7
 Percent Similarity:  80.039   Percent Identity: 58.121
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alignment_block:

US-09-444-711-1 x AAB99332 ..

Align seg 1/1 to: AAB99332 from: 1 to: 505

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  82 GGCGGGGGCGCTTTCCCCGCCTCGCAGACCCCCAGCAAGCCAG....... 124
     ||||||:::::|||      :::::|||    ||||||
  12 GlyGlyAsnThrPheSerLysThrGluThr.SerAlaSerProHisCysP 28

 125 ..........CCTCGGCCGACGGCCACCGCGGCCCCAGCGCGGCCTTCG 163
               |||   ||||||:::|||      |||:::   |||:::
  28 roValTyrValProAspProThrSerThrIleLysProGly...ProAsn 43

 164 CCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTTCAACTCCTCGGAC 213
         :::      :::|||:::      ||||||  :::|||:::|||
  44 SerHisAsnSerAsnThrProGlyIleArgGluAla..GlySerGluAsp 59

 214 ACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTGACCAC 263
       ::::::
  60 IleIleVal..................................... 62

 264 CTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCCT 313
         ||||||||||||||||||:::      :::   ||||||||||
  63 ....ValAlaLeuTyrAspTyrGluAlaIleHisHisGluAspLeuSerP 78

 314 TCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACACGGAGGGAGACTGG 363
     ||:::||||||:::::::::   :::|||   :::   :::|||:::|||
  78 heGlnLysGlyAspGlnMet...ValValLeuGluGluSerGlyGluTrp 93
```

```
     |||||||:::   |||:::::::::|||||   |||||||:::      |
 150 eGlyLysLeuGlyArgLysAspAlaGluArgGlnLeuLeuSerPheGlyA 167

 509 ACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGAAAGGTGCC 558
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 167 snProArgGlyThrPheLeuIleArgGluSerGlnThrThrLysGlyAla 183

 559 TACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTCAACGTGAA 608
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 184 TyrSerLeuSerIleArgAspTrpAspAspMetLysGlyAspHisValLy 200

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 217 rgAlaGln...GluThrLeuGlnGlnLeuValGlnHisTyrSerGluLys 232

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seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-665-647-1

seq_documentation_block:
; Sequence 1, Application US/08665647
; Patent No. 5935803
;  GENERAL INFORMATION:
;    APPLICANT:  Dasquez, Nicki J.
;    APPLICANT:  Ron, Dorit
;    APPLICANT:  Voronova, Anna F.
;    APPLICANT:  Napolitano, Eugene W.
;    TITLE OF INVENTION:  METHODS TO IDENTIFY IMMUNOMODULATORS
;    TITLE OF INVENTION:  USING COGNATE INTERACTION OF PKC-THETA
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW - Ste. 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,647
;      FILING DATE:  18-JUN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22550-20025.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 822-0168
;      TELEX:  90-4030 MRSNFOERSWSH
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  532 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
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;      LOCATION:  1..1002
US-08-665-647-1


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;    TITLE OF INVENTION:  NOVEL MEGAKARYOCYTIC PROTEIN
;    TITLE OF INVENTION:  TYROSINE KINASES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York,
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/426,509A
;      FILING DATE:  21-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/232,545
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-0074-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  537 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  No. 6326469e
US-08-426-509A-11


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             Ratio:  4.201                Gaps:      6
 Percent Similarity:  83.183   Percent Identity: 67.812

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    212 AC...ACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTG 258
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    409 AGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTT 458
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    135 SerAsnTyrValAlaProValAspSerIleGlnAlaGluGluTrpTyrPh 151

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seq_documentation_block:
; Sequence 14, Application US/08426509A
; Patent No. 6326469
;  GENERAL INFORMATION:
;    APPLICANT:  Ullrich,, Axel
;    APPLICANT:  Gishizsky,, Mikhail
;    APPLICANT:  Sures,, Irman G.
;    TITLE OF INVENTION:  NOVEL MEGAKARYOCYTIC PROTEIN
;    TITLE OF INVENTION:  TYROSINE KINASES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York,
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/426,509A
;      FILING DATE:  21-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/232,545
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-0074-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
    NFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  543 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  No. 6326469e
US-08-426-509A-14


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214 eArgLysLeuAspAsnGlyGlyTyrTyrIleThrThrArgAlaGlnPheA 231

671 ACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG 720
231 spThrLeuGlnLysLeuValLysHisTyrThrGluHisAlaAspGlyLeu 247

721 TGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGG 770
248 CysHisLysLeuThrThrValCysProThrValLysProGlnThrGlnGl 264

771 CCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGG 820
264 yLeuAlaLysAspAlaTrpGluIleProArgGluSerLeuArgLeuGluV 281

821 TCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGAAC 870
281 alLysLeuGlyGlnGlyCysPheGlyGluValTrpMetGlyThrTrpAsn 297

871 GGTACCACCAGGGTGGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCC 920
298 GlyThrThrLysValAlaIleLysThrLeuLysProGlyThrMetMetPr 314

921 AGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTGAGGCATGAGA 970
314 oGluAlaPheLeuGlnGluAlaGlnIleMetLysLysLeuArgHisAspL 331

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331 ysLeuValProLeuTyrAlaValValSerGluGluProIleTyrIleVal 347

1021 ACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTTTCTCAAGGGGGAGAC 1070
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364 pGlyLysTyrLeuLysLeuProGlnLeuValAspMetAlaAlaGlnIleA 381

1121 CCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTCCACCGGGACCTT 1170
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1171 CGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTGCAAAGTGGCCGA 1220
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1271 GTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGC 1320
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1321 CGCTTCACCATCAAGTCGGACGTGTGGTCCTTCGGGATCCTGCTGACTGA 1370
 448 ArgPheThrIleLysSerAspValTrpSerPheGlyIleLeuGlnThrGl 464

1371 GCTCACCACAAAGGGACGGGTGCCCTACCCTGGGATGGTGAACCGCGAGG 1420
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1521 GGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGGAGGACTACTTCA 1570
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; Sequence 12, Application US/08426509A
; Patent No. 6326469
;  GENERAL INFORMATION:
;    APPLICANT:  Ullrich,, Axel
;    APPLICANT:  Gishizsky,, Mikhail
;    APPLICANT:  Sures,, Irman G.
;    TITLE OF INVENTION:  NOVEL MEGAKARYOCYTIC PROTEIN
;    TITLE OF INVENTION:  TYROSINE KINASES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York,
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/426,509A
;      FILING DATE:  21-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/232,545
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-0074-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
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seq_name: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US95-05008-12

seq_documentation_block:
; Sequence 12, Application PC/TUS9505008
;  GENERAL INFORMATION:
;    APPLICANT:  Sugen, Inc.
;    APPLICANT:  515 Galveston Drive
;    APPLICANT:  Redwood City, California 94063-4720
;    APPLICANT:  United States of America
;    APPLICANT:  Wissenschaften E.V.
;    APPLICANT:  Hofgarten Str. 2
;    APPLICANT:  Munchen 80539
;    APPLICANT:  Germany
;    TITLE OF INVENTION:  Novel Megakaryocytic Protein Tyrosine
;    TITLE OF INVENTION:  Kinases
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05008
;      FILING DATE:  24-APR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/232,545
;      FILING DATE:  22-APR-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-074
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)790-9090
;      TELEFAX:  (212)869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  536 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
PCT-US95-05008-12


alignment_scores:
            Quality: 1949.00              Length:    528
              Ratio:  4.350                Gaps:      4
 Percent Similarity:  84.848    Percent Identity: 71.023

alignment_block:
 US-09-444-711-1 x PCT-US95-05008-12   ..

 Align seg 1/1  to: PCT-US95-05008-12  from: 1  to: 536

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      24 aHisProProSerGlnTyrAspProAspProThrGlnLeuSerGlyAlaP 41

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     481 TCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTTCCTCGT 530
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     158 AlaGluArgGlnLeuLeuCysHisGlyAsnCysArgGlyThrPheLeuIl 174

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     174 eArgGluSerGluThrThrLysGlyAlaTyrSerLeuSerIleArgAspT 191

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     324 sLeuValGlnLeuTyrAlaValValSerGluGluProIleTyrIleValT 341
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;    APPLICANT:  United States of America
;    APPLICANT:  Wissenschaften E.V.
;    APPLICANT:  Hofgarten Str. 2
;    APPLICANT:  Munchen 80539
;    APPLICANT:  Germany
;    TITLE OF INVENTION:  Novel Megakaryocytic Protein Tyrosine
;    TITLE OF INVENTION:  Kinases
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05008
;      FILING DATE:  24-APR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/232,545
;      FILING DATE:  22-APR-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-074
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)790-9090
;      TELEFAX:  (212)869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  536 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
PCT-US95-05008-13


alignment_scores:
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Db    481 AGGGAAGGTACCAAATTTCCCATCAAGTGGACATCCCTGGAGGCTGCCAATTATGGCTCT 540

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Db    601 GGGAGGACTCCATATCCAGGTATGTCCAACTCGGAGGTAATTACAGCCCTTGAGCGTGGT 660

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Db    661 TATCGCATGCCGTGTCCCAGCACTTGTCCAAAAGAGCTCTACAGCATCATGCTCCAGTGT 720

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RESULT 14
US-09-228-603A-7
; Sequence 7, Application US/09228603A
; Patent No. 6291651
;  GENERAL INFORMATION:
;    APPLICANT:  Hemmati-Brivanlou, Ali
;    APPLICANT:  Weinstein, Daniel C.
;    TITLE OF INVENTION:  A NOVEL SRC-FAMILY KINASE AND METHODS OF
;    TITLE OF INVENTION:  USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/228,603A
;      FILING DATE:  12-JAN-1999
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-217 N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  780 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..780
US-09-228-603A-7

  Query Match            21.2%;  Score 341.6;  DB 4;  Length 780;
  Best Local Similarity  65.8%;  Pred. No. 6.4e-61;
  Matches  513;  Conservative    0;  Mismatches  264;  Indels    3;  Gaps    1;

Qy    787 tgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgctttggc 846
          |||||||||||| || ||||| |||   ||| ||   ||||| ||    ||    |||||
Db      1 TGGGAGATCCCGCGCGAGTCACTGTCACTGCAGAAGAAGCTTGGAGCTGGACAGTTTGGG 60

Qy    847 gaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaagcct 906
          || || ||| |||  |  |  || ||   ||| |  || ||  | |||||  |||||||
Db     61 GATGTTTGGTTGGCCATGTACAATGGACACACAAAAGTAGCTGTAAAAACAATGAAGCCA 120

Qy    907 ggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcat 966
          ||||  ||||| || |  ||||||||  | |||||  |  | |||||||   ||  ||||
Db    121 GGCAGCATGTCCCCCGGTGCCTTCCTTGAAGAGGCAAATCTGATGAAGAGCTTGCAGCAT 180

Qy    967 gagaagctggtgcagttgtatgc---tgtggtttcagaggagcccatttacatcgtcacg 1023
          ||  |||||||| |||| ||||   |||| |   | ||| || || || ||| | ||
Db    181 GACCGGCTGGTGCGGTTGCATGCCGTTGTGACTCAGGGGGAACCAATATATATCATTACT 240

Qy   1024 gagtacatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtacctg 1083
          ||||| |||   ||||| |||||||||||| || || ||  | ||   ||| |   |||
Db    241 GAGTATATGCAAAAGGGCAGTTTGCTGGATTTCCTGAAAAGTGAAGAAGGTAGCGACCAA 300

Qy   1084 cggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggag 1143
          |  |||  ||| ||  | ||| |  |||| ||||| ||   ||| |||  ||   | |||
Db    301 CCTCTGATTCAACTCATTGACTTCTCTGCCCAGATTGCAGAAGGAATGTGGTTTATTGAG 360

Qy   1144 cggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaacctg 1203
          |  | ||| ||  | ||||| || ||  | ||||| |||  ||||||   ||| |   ||
Db    361 CAAAGGAATTATATTCACCGTGATCTGAGGGCAGCAAACTGCCTGGTATCAGAAACTTTG 420

Qy   1204 gtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacggcg 1263
          ||||||||  | || ||||||||||||||| ||  | || || ||||  ||||| || ||
Db    421 TTGTGCAAAATAGCAGACTTTGGGCTGGCCCGAGTGATAGAGGACAGCGAGTATACTGCC 480

Qy   1264 cggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggccgc 1323
           || ||||| ||||||| |||||||||||||||  | |  || ||||||   ||||||
Db    481 AGGGAAGGTACCAAATTTCCCATCAAGTGGACATCCCTGGAGGCTGCCAATTATGGCTCT 540

Qy   1324 ttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccacaaag 1383
          || || |||||||| || || ||||| || ||  |  |||| |||||  | |  ||| |
Db    541 TTTACTATCAAGTCAGATGTATGGTCATTTGGTGTATTGCTAACTGAAATAATAACATAT 600

Qy   1384 ggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcggggc 1443
          ||  ||   || || || || |||   |||   |||||  |        | ||||| ||
Db    601 GGGAGGACTCCATATCCAGGTATGTCCAACTCGGAGGTAATTACAGCCCTTGAGCGTGGT 660

Qy   1444 taccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccagtgc 1503
          || || ||||| || ||       |||||  |    ||  ||  | |||||  ||||||
Db    661 TATCGCATGCCGTGTCCCAGCACTTGTCCAAAAGAGCTCTACAGCATCATGCTCCAGTGT 720

Qy   1504 tggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggaggac 1563
          |||| | |||| |||||| | ||||| || || || ||  | |||  | |||| ||||||
Db    721 TGGCAGCAGGACCCTGAGCAACGGCCAACGTTTGAATATTTACAGAGCATCCTAGAGGAC 780


RESULT 15
US-08-426-509A-5
; Sequence 5, Application US/08426509A
; Patent No. 6326469
;  GENERAL INFORMATION:
;    APPLICANT:  Ullrich,, Axel
;    APPLICANT:  Gishizsky,, Mikhail
;    APPLICANT:  Sures,, Irman G.
;    TITLE OF INVENTION:  NOVEL MEGAKARYOCYTIC PROTEIN
;    TITLE OF INVENTION:  TYROSINE KINASES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
```

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Db    807 TGCCTTCCTTGAAGAGGCAAATCTGATGAAGAGCTTGCAGCATGACCGGCTGGTGCGGTT 866

Qy    984 gtatgc---tgtggtttcagaggagcccatttacatcgtcacggagtacatgagcaaggg 1040
Db    867 GCATGCCGTTGTGACTCAGGGGGAACCAATATATATCATTACTGAGTATATGCAAAAGGG 926

Qy   1041 gagtttgctggactttctcaaggggggagacaggcaagtacctgcggctgcctcagctggt 1100
Db    927 CAGTTTGCTGGATTTCCTGAAAAGTGAAGAAGGTAGCGACCAACCTCTGATTCAACTCAT 986

Qy   1101 ggacatggctgctcagatcgcctcaggcatggcgtacgtggagcggatgaactacgtcca 1160
Db    987 TGACTTCTCTGCCCAGATTGCAGAAGGAATGTGGTTTATTGAGCAAAGGAATTATATTCA 1046

Qy   1161 ccgggaccttcgtgcagccaacatcctggtgggagagaacctggtgtgcaaagtggccga 1220
Db   1047 CCGTGATCTGAGGGCAGCAAACTGCCTGGTATCAGAAACTTTGTTGTGCAAAATAGCAGA 1106

Qy   1221 ctttgggctggctcggctcattgaagacaatgagtacacggcgcggcaaggtgccaaatt 1280
Db   1107 CTTTGGGCTGGCCCGAGTGATAGAGGACAGCGAGTATACTGCCAGGGAAGGTACCAAATT 1166

Qy   1281 ccccatcaagtggacggctccagaagctgccctctatggccgcttcaccatcaagtcgga 1340
Db   1167 TCCCATCAAGTGGACATCCCTGGAGGCTGCCAATTATGGCTCTTTTACTATCAAGTCAGA 1226

Qy   1341 cgtgtggtccttcgggatcctgctgactgagctcaccacaaagggacgggtgccctaccc 1400
Db   1227 TGTATGGTCATTTGGTGTATTGCTAACTGAAATAATAACATATGGGAGGACTCCATATCC 1286

Qy   1401 tgggatggtgaaccgcgaggtgctggaccaggtggagcggggctaccggatgccctgccc 1460
Db   1287 AGGTATGTCCAACTCGGAGGTAATTACAGCCCTTGAGCGTGGTTATCGCATGCCGTGTCC 1346

Qy   1461 gccggagtgtcccgagtccctgcacgacctcatgtgccagtgctggcggaaggagcctga 1520
Db   1347 CAGCACTTGTCCAAAAGAGCTCTACAGCATCATGCTCCAGTGTTGGCAGCAGGACCCTGA 1406

Qy   1521 ggagcggcccaccttcgagtacctgcaggccttcctggaggactacttcacgtccaccga 1580
Db   1407 GCAACGGCCAACGTTTGAATATTTACAGAGCATCCTAGAGGACTTCTTTACTGCCACTGA 1466

Qy   1581 gccccagtaccagcc 1595
Db   1467 AACACAGTACCAGGC 1481


RESULT 11
US-09-173-581-12
; Sequence 12, Application US/09173581A
; Patent No. 6013455
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Hillman, Jennifer L.
;  APPLICANT: Yue, Henry
;  APPLICANT: Guegler, Karl J.
;  APPLICANT: Corley, Neil C.
;  APPLICANT: Gorgone, Gina
;  APPLICANT: Azimzai, Yalda
;  APPLICANT: Lu, Aina
;  TITLE OF INVENTION: Protein Kinase Homologs
;  FILE REFERENCE: PF-0614 US
;  CURRENT APPLICATION NUMBER: US/09/173,581A
;  CURRENT FILING DATE: 1998-10-15
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PERL Program
; SEQ ID NO 12
;  LENGTH: 1574
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE: -
;  OTHER INFORMATION: 507669
US-09-173-581-12


  Query Match             21.5%;  Score 346.2;  DB 3;  Length 1574;
  Best Local Similarity   70.1%;  Pred. No. 8.5e-62;
  Matches  465;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy    933 gcaggaggcccaggtcatgaagaagctgaggcatgagaagctggtgcagttgtatgctgt 992
Db    464 gcccgaggccaacctcatgaagcagctgcaacaccagcggctggttcggctctacgctgt 523

Qy    993 ggtttcagaggagcccatttacatcgtcacggagtacatgagcaaggggagtttgctgga 1052
Db    524 ggtcacccaggagcccatctacatcatcactgaatacatggagaatgggagtctagtgga 583

Qy   1053 ctttctcaaggggggagacaggcaagtacctgcggctgcctcagctggtggacatggctgc 1112
Db    584 ttttctcaagacccctcaggcatcaagttgaccatcaacaaactcctggacatggcagc 643

Qy   1113 tcagatcgcctcaggcatggcgtacgtggagcggatgaactacgtccaccgggaccttcg 1172
Db    644 ccaaattgcagaaggcatggcattcattgaagagcggaattatattcatcgtgaccttcg 703

Qy   1173 tgcagccaacatcctggtgggagagaacctggtgtgcaaagtggccgactttgggctggc 1232
Db    704 ggctgccaacattctggtgtctgacaccctgagctgcaagattgcagactttggcctagc 763

Qy   1233 tcggctcattgaagacaatgagtacacggcgcggcaaggtgccaaattccccatcaagtg 1292
Db    764 acgcctcattgaggacaacgagtacacagccagggaggggccaagtttcccattaagtg 823

Qy   1293 gacggctccagaagctgccctctatggccgcttcaccatcaagtcggacgtgtggtcctt 1352
Db    824 gacagcgccagaagccattaactacgggacattcaccatcaagtcagatgtgtggtcttt 883

Qy   1353 cgggatcctgctgactgagctcaccacaaagggacgggtgccctaccctgggatggtgaa 1412
Db    884 tgggatcctgctgacggaaattgtcacccacggccgcatcccttacccagggatgaccaa 943

Qy   1413 ccgcgaggtgctggaccaggtggagcggggctaccggatgccctgcccgccggagtgtcc 1472
Db    944 cccggaggtgattcagaacctggagcgaggctaccgcatggtgcgccctgacaactgtcc 1003

Qy   1473 cgagtccctgcacgacctcatgtgccagtgctggcggaaggagcctgaggagcggcccac 1532
Db   1004 agaggagctgtaccaactcatgaggctgtgctggaaggagcgcccagaggaccggcccac 1063

Qy   1533 cttcgagtacctgcaggccttcctggaggactacttcacgtccaccgagccccagtacca 1592
Db   1064 ctttgactacctgcgcagtgtgctggaggacttcttcacggccacagagggccagtacca 1123

Qy   1593 gcc 1595
Db   1124 gcc 1126


RESULT 12
US-09-420-915-12
; Sequence 12, Application US/09420915
; Patent No. 6264947
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Hillman, Jennifer L.
;  APPLICANT: Yue, Henry
;  APPLICANT: Guegler, Karl J.
;  APPLICANT: Corley, Neil C.
;  APPLICANT: Gorgone, Gina
;  APPLICANT: Azimzai, Yalda
;  APPLICANT: Lu, Aina
;  TITLE OF INVENTION: Protein Kinase Homologs
;  FILE REFERENCE: PF-0614 US
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Qy    892 aaaaccctgaagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatg 951
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Db   1067 AAAACACTAAAACCAGGTACAATGATGCCAGAAGCTTTTCTTCAAGAAGCTCAGGTAATG 1126

Qy    952 aagaagctgaggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatt 1011
          || ||  | || ||||  || || || |  | |||||||| ||||| || |||| |||
Db   1127 AAAAAAATAAGACATGGTAAACTTGTTCCACTATATGCTGTTGTTTCTGAAGAGCCAATT 1186

Qy   1012 tacatcgtcacggagtacatgagcaaggggagtttgctggactttctcaagggggagaca 1071
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Db   1187 TACATTGTCACTGAATTGATGTCAAAAGGAAGCTTATTCAATTTCCTTAAGGAAGGAGAT 1246

Qy   1072 ggcaagtacctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatg 1131
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Db   1247 GGAAAGTATTTGAAGCTTCCACAAATGGTTGATATGCCTGCTCAGATTGCTGATGGTATG 1306

Qy   1132 gcgtacgtggagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtg 1191
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Db   1307 GCATATATTAAAAGAATGAACTATATTCACCGAGATCTCTGGGCTGCTAATATTCTTGTA 1366

Qy   1192 ggagagaacctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaat 1251
          ||||| || ||  |||||||| | || || |||||  | ||  || | ||||||||||||
     1367 GGAGAAAATCTTCTGTGCAAAATAGCAGATTTTGGTTTAGCAAGGTTAATTGAAGACAAT 1426

Qy   1252 gagtacacggcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgcc 1311
          || |||||  |  | ||||||||  |||| || ||||| ||||| ||||| |||| |||
Db   1427 GAATACACATCAAGACAAGGTGCAGAATTTCCAATCAAATGGACAGCTCCTGAAGTTGCA 1486

Qy   1312 ctctatggccgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgag 1371
          || |||||  | || || || ||||| |  || || || || || || || | ||| ||
Db   1487 CTGTATGGTGGGTTTACAATAAAGTCTGGTGTCTGCTCATTTGGAATTCTACAGACAGAA 1546

Qy   1372 ctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccag 1431
          ||     |||||||| | ||||| || || || |||||||||| ||  | ||||| |||
Db   1547 CTGGTAACAAAGGGCAGAGTGCCATATCCAGGTATGGTGAACCATGAAATACTGGAACAG 1606

Qy   1432 gtggagcggggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctc 1491
          |||||||| || ||| ||||||| ||||| | ||  ||||| || ||||| || ||  |
Db   1607 GTGGAGCGAGGATACAGGATGCCTTGCCCTCAGGGCTGTCCAGAATCCCTCCATGAATTG 1666

Qy   1492 atgtgccagtgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggcc 1551
          |||  | ||| |||  |||||| ||||| ||  | || || || || || ||  | ||| ||
Db   1667 ATGAATCTGTGTTGGAAGAAGGACCCTGATGAAAGACCAACATTTGAATATGTTCAGTCC 1726

Qy   1552 ttcctggaggactacttcacgtccaccgagccccagtaccagcccggggagaacctcta 1610
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Db   1727 TTCTTGGGAGACTACTTCACTGCTACAGAGCCATAGTACCAGCCAGGAGAAAACTTCTA 1785
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RESULT   9
    9-006-675-1
; Sequence 1, Application US/09006675
; Patent No. 5952213
;  GENERAL INFORMATION:
;    APPLICANT:  Hemmati-Brivanlou, Ali
;    APPLICANT:  Weinstein, Daniel C.
;    TITLE OF INVENTION:  A NOVEL SRC-FAMILY KINASE AND METHODS OF
;    TITLE OF INVENTION:  USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/006,675
;      FILING DATE:  13-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-217
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1491
US-09-006-675-1


  Query Match             28.9%;  Score 465.8;  DB 2;  Length 1491;
  Best Local Similarity   61.6%;  Pred. No. 5.2e-86;
  Matches  822;  Conservative    0;  Mismatches  492;  Indels   21;  Gaps    4;

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          | |  |||| | ||||||||||                 || ||| | || | ||||||
Db    165 CCTGCTGGCTTTGTATGACTATGATGGAGTCCACCCTGGGGATCTGACTTTTAGGAAAGG 224

Qy    324 cgagcggctccagattgtcaacaacacggagggagactggtggctggcccactcgctcag 383
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Db    225 GGACCATCTCC---TGCTAAAGAAAGAGTCAGGGGAGTGGTGGGAAGCATGTCTAATTTC 281

Qy    384 cacaggacagacaggctacatccccagcaactacgtggcgccctccgactccatccaggc 443
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Db    282 CACTGGTGAAGAAGGCTTTGTTCCCAGTAACTATGTAGCGTATTTCAATTCCCTGGAATC 341

Qy    444 tgaggagtggtattttggcaagatcaccagacgggagtcagagcggttactgctcaatgc 503
          ||| |||||||| |||      || | | |   ||| | ||  ||   |||||   | |
Db    342 TGAAGAGTGGTACTTTAAAGGCATGAGCCGGAAGGAAGCTGAAAGGCAGCTGCTATCTCC 401

Qy    504 agagaacccgagagggaccttcctcgtgcgagaaagtgagaccacgaaaggtgcctactg 563
          |  ||   || ||| | ||| |  | ||||| |||||||| | |||||||   | ||
Db    402 TGTTAATAAAAGTGGGGCTTTCATGATCCGAGACAGTGAGACAATGAAAGGTTGTTTCTC 461

Qy    564 cctctcagtgtctgacttcgacaacgccaagggcctcaacgtgaagcactacaagatccg 623
          |||||| |||   ||||             ||   ||  ||||| || ||||| || ||
Db    462 CCTCTCTGTGCGAGACT-----------CAGGGGACACTGTGAAACATTACAAAATTCG 509

Qy    624 caagctggacagcggcggcttctacatcacctcccgcacccagttcaacagcctgcagca 683
          || || ||    || || |||| ||| | | || | ||  ||         |||  |
Db    510 CACACTCGATGATGGAGGTTTCTTCATTTCTACACGGATCCCTTTTCCTTCTTTGCCAGA 569

Qy    684 gctggtggcctactactccaaacacgccgatggcctgtgccaccgcctcaccaccgtgtg 743
          ||||||   | | ||        | |  |||||| |||| ||  |||| || |    ||
Db    570 GCTGGTACGCCATTATCAAGGTAAAGTGGATGGCTTGTGTCAGTGCCTTACAATACCATG 629

Qy    744 ccccacgtccaagccgcagactcagggcctggccaaggatgcctgggagatccctcggga 803
          ||  ||       ||  ||| |  |   ||  ||||||||||||||||||| || ||
Db    630 CCAAACTGTGCGTCCAGAGAAACCATG---GGAAAAGGATGCCTGGGAGATCCCGCGCGA 686

Qy    804 gtcgctgcggctggaggtcaagctgggccagggctgctttggcgaggtgtggatggggac 863
          ||| |||   ||| ||   |||| ||    ||  |||| || || ||| ||| |
Db    687 GTCACTGTCACTGCAGAAGAAGCTTGGAGCTGGACAGTTTGGGGATGTTTGGTTGGCCAT 746

Qy    864 ctggaacggtaccaccagggtggccatcaaaaccctgaagcctggcacgatgtctccaga 923
          |  || ||   ||| |  || ||  | |||||  ||||||| ||||  |||| || |
Db    747 GTACAATGGACACACAAAAGTAGCTGTAAAAACAATGAAGCCAGGCAGCATGTCCCCCGG 806
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Db    781 GATGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGC 840

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Db    841 TTTGGCGAGGTGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900

Qy    901 aagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctg 960
Db    901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTG 960

Qy    961 aggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtc 1020
Db    961 AGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTC 1020

Qy   1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtac 1080
Db   1021 ACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTTTCTCAAGGGGAGACAGGCAAGTAC 1080

Qy   1081 ctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtg 1140
Db   1081 CTGCGGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTG 1140

     1141 gagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaac 1200
Db   1141 GAGCGGATGAACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1200

Qy   1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260
Db   1201 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAATGAGTACACG 1260

Qy   1261 gcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggc 1320
Db   1261 GCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGC 1320

Qy   1321 cgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccaca 1380
Db   1321 CGCTTCACCATCAAGTCGGACGTGTGGTCCTTCGGGATCCTGCTGACTGAGCTCACCACA 1380

Qy   1381 aagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcgg 1440
Db   1381 AAGGGACGGGTGCCCTACCCTGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGG 1440

Qy   1441 ggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccag 1500
Db   1441 GGCTACCGGATGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAG 1500

Qy   1501 tgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggag 1560
Db   1501 TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGGAG 1560

     1561 gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag 1611
Db   1561 GACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGGAGAACCTCTAG 1611
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RESULT   3
US-07-820-011A-1
; Sequence 1, Application US/07820011A
; Patent No. 5336615
;  GENERAL INFORMATION:
;    APPLICANT:  Bell, Leonard
;    APPLICANT:  Madri, Joseph A.
;    APPLICANT:  Warren, Stephen L.
;    APPLICANT:  Luthringer, Daniel J.
;    TITLE OF INVENTION:  Genetically Engineered
;    TITLE OF INVENTION:  Endothelial Cells Exhibiting Enhanced
;    TITLE OF INVENTION:  Migration
;    TITLE OF INVENTION:  and Plasminogen Activator Activity
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairifield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb storage
;      COMPUTER:  IBM PC XT
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 2.10
;      SOFTWARE:  Displaywrite 3
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/820,011A
;      FILING DATE:  19920106
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  LB-101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255 1400
;      TELEFAX:  (203) 254 1101
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1602 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Gallus, gallus
;    PUBLICATION INFORMATION:
;      AUTHORS:  Takeya, Tatsuo
;      AUTHORS:  Hanafusa, Hidesaburo
;      TITLE:  Structure and Sequence of the
;      TITLE:  Cellular Gene Homologous to the RSV src
;      TITLE:  Gene and the Mechanism for Generating the
;      TITLE:  Transforming Virus
;      JOURNAL:  Cell
;      VOLUME:  32
;      PAGES:  881-890
;      DATE:  March, 1983
US-07-820-011A-1


  Query Match             75.5%;  Score 1216.6;  DB 1;  Length 1602;
  Best Local Similarity   85.2%;  Pred. No. 5.9e-238;
  Matches 1373;  Conservative    0;  Mismatches  229;  Indels    9;  Gaps    1;

Qy      1 atgggtagcaacaagagcaagcccaaggatgccagccagcggcgccgcagcctggagccc 60
Db      1 ATGGGGAGCAGCAAGAGCAAGCCCAAGGACCCCAGCCAGCGCCGGCGCAGCCTGGAGCCA 60

Qy     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120
Db     61 CCCGACAGCACCCACCAC---------GGGGGATTCCCAGCCTCGCAGACCCCCAACAAG 111

Qy    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgcccccgcggccgccgag 180
Db    112 ACAGCAGCCCCCGACACGCACCGCACCCCCAGCCGCTCCTTTGGGACCGTGGCCACCGAG 171

Qy    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240
Db    172 CCCAAGCTCTTCGGGGGCTTCAACACTTCTGACACCGTTACGTCGCCGCAGCGTGCCGGG 231

Qy    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300
Db    232 GCACTGGCTGGCGGCGTCACCACTTTCGTGGCTCTCTACGACTACGAGTCCCGGACTGAA 291

Qy    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagac 360
Db    292 ACGGACTTGTCCTTCAAGAAAGGAGAACGCCTGCAGATTGTCAACAACACGGAAGGTGAC 351
```

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;    PUBLICATION INFORMATION:
;      AUTHORS:  Anderson, Stephen K.
;      AUTHORS:  Gibbs, Carol P.
;      AUTHORS:  Tanaka, Akio
;      AUTHORS:  Kung, Hsing-Jien
;      AUTHORS:  Fujita, Donald J.
;      TITLE:  Human Cellular src Gene:
;      TITLE:  Nucleotide Sequence and Derived Amino
;      TITLE:  Acid Sequence of the Region Coding for
;      TITLE:  the Carboxy-Terminal Two-Thirds of
;      TITLE:  pp60c-src
;      JOURNAL:  Molecular and Cellular Biology
;      VOLUME:  5
;      ISSUE:  5
;      PAGES:  1122-1129
;      DATE:  May, 1985
;    PUBLICATION INFORMATION:
;      AUTHORS:  Tanaka, Akio
;      AUTHORS:  Gibbs, Carol P.
;      AUTHORS:  Arthur, Richard R.
;      AUTHORS:  Anderson, Stephen K.
;      AUTHORS:  Kung, Hsing-Jien
;      AUTHORS:  Fujita, Donald J.
;      TITLE:  DNA Sequence Encoding the
;      TITLE:  Amino-Terminal Region of the Human c-src
;      TITLE:  Protein: Implications of Sequence
;      TITLE:  Divergence among src-Type Kinase
;      TITLE:  Oncogenes
;      JOURNAL:  Molecular and Cellular Biology
;      VOLUME:  7
;      ISSUE:  5
;      PAGES:  1978-1983
;      DATE:  May, 1987
US-07-820-011A-3

  Query Match           99.9%;  Score 1609.4;  DB 1;  Length 1611;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1610;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 atgggtagcaacaagagcaagcccaaggatgccagccagcggcgccgcagcctggagccc 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGGTAGCAACAAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAGCCTGGAGCCC 60

Qy     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCGCCTCGCAGACCCCCAGCAAG 120

Qy    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgcccccgcggccgccgag 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCAGCCTCGGCCGACGGCCACCGCGGCCCCAGCGCGGCCTTCGCCCCCGCGGCCGCCGAG 180

Qy    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCAAGCTGTTCGGAGGCTTCAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGC 240

Qy    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCGCTGGCCGGTGGAGTGACCACCTTTGTGGCCCTCTATGACTATGAGTCTAGGACGGAG 300

Qy    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagac 360
          ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACACAGAGGGAGAC 360

Qy    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCCAGCAACTACGTG 420

Qy    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAG 480

Qy    481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGT 540

Qy    541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGACCACGAAAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600

Qy    601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGC 660

Qy    661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG 720

Qy    721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGGCCTGGCCAAG 780

Qy    781 gatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GATGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGC 840

Qy    841 tttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTTGGCGAGGTGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900

Qy    901 aagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTG 960

Qy    961 aggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtc 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTC 1020

Qy   1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggggagacaggcaagtac 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTTTCTCAAGGGGGAGACAGGCAAGTAC 1080

Qy   1081 ctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtg 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CTGCGGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTG 1140

Qy   1141 gagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaac 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GAGCGGATGAACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1200

Qy   1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAATGAGTACACG 1260

Qy   1261 gcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggc 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGC 1320

Qy   1321 cgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccaca 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CGCTTCACCATCAAGTCGGACGTGTGGTCCTTCGGGATCCTGCTGACTGAGCTCACCACA 1380

Qy   1381 aagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcgg 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AAGGGACGGGTGCCCTACCCTGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGG 1440

Qy   1441 ggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccag 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GGCTACCGGATGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAG 1500

Qy   1501 tgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGGAG 1560

Qy   1561 gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag 1611
          |||||||||||||||||||||||||||||||||||||||||||||||||
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PT   - targetting cytoplasmic and nuclear oncogene(s)
XX
PS   Claim 1; Column 111-112; 92pp; English.
XX
CC   The present sequence represents an oncogene from the present invention.
CC   The present invention describes a composition which comprises two
CC   antisense oligonucleotides. The first oligonucleotide is specific for a
CC   cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1,
CC   c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and
CC   c-yes. The second oligonucleotide is specific for a nuclear oncogene or
CC   proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb,
CC   c-rel, c-vav, c-ski, c-spi, cyclin D1, PML/RAR alpha , AML1/MTG8,
CC   E2A/prl and ALL-1/AF-4. The composition is used for treating cancer.
CC   The combination of antisense oligonucleotides has synergistically
CC   enhanced ability to inhibit growth of cancer cells.
XX
SQ   Sequence 1804 BP; 595 A; 331 C; 428 G; 450 T; 0 other;


  Query Match             33.5%;  Score 539.8;  DB 19;  Length 1804;
  Best Local Similarity   68.8%;  Pred. No. 7.8e-93;
  Matches  742;  Conservative    0;  Mismatches  337;  Indels    0;  Gaps    0;

Qy     532 cgagaaagtgagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgcc 591
           ||||| || || || || |||||||| || | ||||||  |   ||| |  ||  | |
Db     707 cgagagagcgaaactactaaaggtgcttattccctctctattcgtgattgggatgaggta 766

Qy     592 aagggcctcaacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatc 651
           | |||   ||| ||||| ||| |||| ||  | || || |||  ||  | | ||| |||
Db     767 aggggtgacaatgtgaaacaccacaaaattaggaaacttgacaatggtagatactatatc 826

Qy     652 acctcccgcacccagttcaacagcctgcagcagctggtggcctactactccaaacacgcc 711
           ||  || |    ||  |  | |  |||||| |  |||      ||||| |  |||| ||
Db     827 acaaccagagaacaacttgatactctgcagaaattggcaaaacactacacagaacatgct 886

Qy     712 gatggcctgtgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggc 771
           |||||  | ||||||    | || || ||||| || ||    || || |||| ||| ||
Db     887 gatggtttatgccacaagttaacaactgtgtgtccaactgtgaaacctcagattcaaggt 946

Qy     772 ctggccaaggatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggc 831
           || || || ||||| ||||| ||||||  |  | ||  |||| || ||||| || || ||
Db     947 ctagcaaaagatgcttgggaaatcccttgataatctttgcgactagaggttaaactagga 1006

Qy     832 cagggctgctttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatc 891
           || || || |||||| | |||||||||||| |  ||||| || ||||| |  || || |||
Db    1007 caaggatgttttggcaaagtgtggatgggaatatggaatggaaccacaaaagtagcaatc 1066

Qy     892 aaaaccctgaagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatg 951
           ||||| || || || || || |||   ||||| || || || || || || ||||| |||
Db    1067 aaaacactaaaaccaggtacaatgatgccagaagcttttcttcaagaagctcaggtaatg 1126

Qy     952 aagaagctgaggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatt 1011
           || ||  | || ||||  || || || |   | |||||||| ||||| || ||||| |||
Db    1127 aaaaaaataagacatggtaaacttgttccactatatgctgttgtttctgaagagccaatt 1186

Qy    1012 tacatcgtcacggagtacatgagcaaggggagtttgctggactttctcaaggggagaca 1071
           ||||| ||||| || |  |||   || || || ||  |  | || || ||||  |
Db    1187 tacattgtcactgaattgatgtcaaaaggaagcttattcaatttccttaaggaaggagat 1246

Qy    1072 ggcaagtacctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatg 1131
           || |||||  ||  ||| || ||  |||| || ||| |||||||||| ||    || |||
Db    1247 ggaaagtatttgaagcttccacaaatggttgatatgcctgctcagattgctgatggtatg 1306

Qy    1132 gcgtacgtggagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtg 1191
           || ||  |  |  | ||||||||  | ||||| || ||  | || || || || || ||
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Qy    1192 ggagagaacctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaat 1251
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Db    1367 ggagaaaatcttctgtgcaaaatagcagattttggtttagcaaggttaattgaagacaat 1426

Qy    1252 gagtacacggcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgcc 1311
           || |||||  |  | |||||||| |||| || ||||| ||||| ||||| |||| |||

Db    1427 gaatacacatcaagacaaggtgcagaatttccaatcaaatggacagctcctgaagttgca 1486

Qy    1312 ctctatggccgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgag 1371
           || |||||  | || || || ||||| |  || || || || || || || | ||| ||
Db    1487 ctgtatggtgggtttacaataaagtctggtgtctgctcatttggaattctacagacagaa 1546

Qy    1372 ctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccag 1431
           ||    |||||||| | ||||| || || || |||||||||| ||  | ||||| |||
Db    1547 ctggtaacaaagggcagagtgccatatccaggtatggtgaaccatgaaatactggaacag 1606

Qy    1432 gtggagcggggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctc 1491
           |||||||| || ||| ||||||| ||||| | ||  ||||| || ||||| || ||  |
Db    1607 gtggagcgaggatacaggatgccttgccctcagggctgtccagaatccctccatgaattg 1666

Qy    1492 atgtgccagtgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggcc 1551
           |||   | ||| |||  |||||| ||||| ||  | || || || || || ||  | ||| ||
Db    1667 atgaatctgtgttggaagaaggaccctgatgaaagaccaacatttgaatatgttcagtcc 1726

Qy    1552 ttcctggaggactacttcacgtccaccgagccccagtaccagcccggggagaacctcta 1610
           ||| |||  |||||||||||  | || ||||  |||||||||| || || ||| ||||
Db    1727 ttcttgggagactacttcactgctacagagccatagtaccagccaggagaaaacttcta 1785


RESULT  15
AAZ60825
ID   AAZ60825 standard; DNA; 1804 BP.
XX
AC   AAZ60825;
XX
DT   16-MAY-2000  (first entry)
XX
DE   Nucleotide sequence of a cognate transgene of c-yes.
XX
KW   Cognate transgene; CTG; tumourigenic; cellular immunogen; immunisation;
KW   proto-oncogene; malignanacy; allogenic cell; vaccine; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200004927-A1.
XX
PD   03-FEB-2000.
XX
PF   08-JUL-1999;   99WO-US15594.
XX
PR   24-JUL-1998;   98US-0093965.
XX
PA   (UYAL-) UNIV ALLEGHNEY HEALTH SCI.
PA   (HALP/) HALPERN M S.
PA   (ENGL/) ENGLAND J M.
XX
PI   Halpern MS,  England JM;
XX
DR   WPI; 2000-182543/16.
XX
PT   Cellular immunogens comprising allogenic donor cells transfected with a
PT   construct comprising a proto-oncogene cognate, useful as cancer
PT   vaccines -
XX
PS   Disclosure; Page 76; 77pp; English.
XX
CC   The present sequence represents a cognate transgene (CTG) which is
CC   rendered non-tumourigenic by deletion of amino acids 9-155. The CTG
CC   is used in the course of the invention. The specification describes a
CC   cellular immunogen for immunizing a host against the effects of the
CC   product of a target proto-oncogene which is associated with a
CC   malignanacy. The cellular immunogen comprises allogenic cells
CC   transfected with transgene construct comprising a transgene cognate
CC   to target proto-oncogene and a strong promoter. The cellular immunogen
CC   is useful for vaccinating a host against cancer by inserting the
CC   transgene construct into the body of the host for the expression of
CC   the transgene. The method of the invention is designed to target
CC   mutation-driven non-self determinants. The cellular immunogens induce
CC   reactivity for self-determinants in the over expressed product of tumour
```

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XX
PI   Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V, Tasken K;
PI   Vang T, Altman A, Munshi A;
XX
DR   WPI; 2000-086801/07.
DR   P-PSDB; AAY49420.
XX
PT   Altering the activity of protein kinase signaling pathways, used for
PT   treating immunosuppressive disorders, e.g. AIDS, proliferative
PT   disorders, e.g. cancers or autoimmune diseases
XX
PS   Claim 22; Page 94-95; 111pp; English.
XX
CC   The invention provides a novel method of altering the activity of the
CC   protein kinase A (PKA) signaling pathway in a cell that comprises
CC   altering the extent of phosphorylation of one or more PKA substrates, or
CC   kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC   compositions containing a nucleic acid molecule that encodes a PKA
CC   substrate, or fragment, precursor or functionally equivalent variant,
CC   where the sequence is modified to alter its susceptibility to
CC   phosphorylation by PKA can be used for treating a disorder exhibiting
CC   abnormal PKA signaling activity, immunosuppressive disorders or
C    proliferative diseases. They can be used for treating e.g. HIV
C    infection, AIDS, common variable immunodeficiency or cancers. Conditions
CC   in which upregulation of the PKA pathway is required, such as autoimmune
CC   disease, e.g. systemic lupus erythematosus, may also be treated. The
CC   present sequence represents a DNA sequence encoding a PKA substrate,
CC   wherein the substrate is in the Src-family, preferably Lck, Fyn, Src,
CC   Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl, Fyk, Src-1 or Src-2.
XX
SQ   Sequence 2032 BP; 450 A; 576 C; 584 G; 422 T; 0 other;

  Query Match             35.7%;  Score 574.8;  DB 21;  Length 2032;
  Best Local Similarity   65.6%;  Pred. No. 2e-99;
  Matches  872;  Conservative    0;  Mismatches  452;  Indels    6;  Gaps    2;

Qy    266 ttgtggccctctatgactatgagtctaggacggagacagacctgtccttcaagaaaggcg 325
          || | || ||  |   ||||||| |       ||   ||| |||  |||  |||| || |
Db    248 ttatcgctctgcacagctatgagccctctcacgacggagatctgggctttgagaaggggg 307

Qy    326 agcggctccagattgtcaacaacacggagggagactggtggctggcccactcgctcagca 385
          | |  ||||  ||  |  |  |   |   || || ||||||  ||| || || || | ||
Db    308 aaccactccgcatcctggagca---gagcggcgagtggtggaaggcgcagtccctgacca 364

Qy    386 caggacagacaggctacatccccagcaactacgtggcgccctccgactccatccaggctg 445
          | || |||  ||||| |||||||  ||| |  |||||     |  ||  | |  || | |
Db    365 cgggccaggaaggcttcatccccttcaattttgtggccaaagcgaacagcctggagcccg 424

Qy    446 aggagtggtattttggcaagatcaccagacgggagtcagagcggttactgctcaatgcag 505
          |   ||||  ||    ||  | | |   |||  | ||||||   || ||     | |
Db    425 aaccctggttcttcaagaacctgagccgcaaggacgcggagcggcagctcctggcgcccg 484

Qy    506 agaacccgagagggaccttcctcgtgcgagaaagtgagaccacgaaaggtgcctactgcc 565
          ||||  |    ||  |||||||| |  || || || |||| |||    ||  |||  |  |
Db    485 ggaacactcacggctccttcctcatccgggagagcgagagcaccgccgggtccttttcac 544

Qy    566 tctcagtgtctgacttcgacaacgccaagggcctcaacgtgaagcactacaagatccgca 625
          | || ||    |||||||| |   | ||||       ||||| || ||||||||||| |
Db    545 tgtcggtccgggacttcgaccaaaaccagggagaggtggtgaaacattacaagatccgta 604

Qy    626 agctggacagcggcggcttctacatcacctcccgcacccagttcaacagcctgcagcagc 685
          | ||||||| ||| |||||||||||| || | || | |   ||   | |||||||  | |
Db    605 atctggacaacggtggcttctacatctcccctcgaatcacttttcccggcctgcatgaac 664

Qy    686 tggtggcctactactccaaacacgccgatggcctgtgccaccgcctcaccaccgtgtgcc 745
          ||||   | | ||| ||||     | ||||| ||||||   ||  | | |  |   ||||
Db    665 tggtccgccattacaccaatgcttcagatgggctgtgcacacggttgagccgcccctgcc 724

Qy    746 ccacgtccaagccgcagactcagggcctggccaaggatgcctgggagatccctcgggagt 805
            ||   ||||| ||||  | | |   ||  |||| |  |||||| | ||  |||||
Db    725 agacccagaagccccagaagccgtggtggg---aggacgagtgggaggttcccagggaga 781

Qy    806 cgctgcggctggaggtcaagctgggccagggctgctttggcgaggtgtggatggggacct 865
          |||||  ||||| ||    ||||||    |     || || ||||||||||||||||  ||
Db    782 cgctgaagctggtggagcggctgggggctgcacagttcggggaggtgtggatggggtact 841

Qy    866 ggaacggtaccaccagggtggccatcaaaaccctgaagcctggcacgatgtctccagagg 925
            |||||   ||| | ||||||  | || | ||||||||  ||||  |||||  || || |
Db    842 acaacgggcacacgaaggtggcggtgaagagcctgaagcagggcagcatgtccccggacg 901

Qy    926 ccttcctgcaggaggcccaggtcatgaagaagctgaggcatgagaagctggtgcagttgt 985
          ||||||||   ||||||  | ||||||| |||||   ||  ||  ||||||  | | | |
Db    902 ccttcctggccgaggccaacctcatgaagcagctgcaacaccagcggctggttcggctct 961

Qy    986 atgctgtggtttcagaggagcccatttacatcgtcacggagtacatgagcaaggggagtt 1045
          | ||||||||  |  ||||||||||| |||||| |||| || ||||||   || ||||||
Db    962 acgctgtggtcacccaggagcccatctacatcatcactgaatacatggagaatgggagtc 1021

Qy   1046 tgctggactttctcaaggggggagacaggcaagtacctgcggctgcctcagctggtggaca 1105
          |  |||| |||||||||       ||||||   |  ||    |      | ||  ||||||
Db   1022 tagtggattttctcaagacccctcaggcatcaagttgaccatcaacaaactcctggaca 1081

Qy   1106 tggctgctcagatcgcctcaggcatggcgtacgtggagcggatgaactacgtccaccggg 1165
          ||||  ||  ||  ||  ||   |||||||||  | | |  ||   |  |||  ||  | ||  |
Db   1082 tggcagcccaaattgcagaaggcatggcattcattgaagagcggaattatattcatcgtg 1141

Qy   1166 accttcgtgcagccaacatcctggtgggagagaacctggtgtgcaaagtggccgactttg 1225
          |||||||  ||  |||||||| ||||||   ||  |  ||||   |||||  |  ||  |||||||
Db   1142 accttcgggctgccaacattctggtgtctgacaccctgagctgcaagattgcagactttg 1201

Qy   1226 ggctggctcggctcattgaagacaatgagtacacggcgcggcaaggtgccaaattcccca 1285
          | ||  ||  ||  |||||||| |||||  |||||||| ||   ||  |  ||  ||||| ||  ||||
Db   1202 gcctagcacgcctcattgaggacaacgagtacacagccagggaggggggccaagtttccca 1261

Qy   1286 tcaagtggacggctccagaagctgccctctatggccgcttcaccatcaagtcggacgtgt 1345
          | ||||||||  ||  ||||||||       |||  ||     ||||||||||||||  ||  ||||
Db   1262 ttaagtggacagcgccagaagccattaactacgggacattcaccatcaagtcagatgtgt 1321

Qy   1346 ggtccttcgggatcctgctgactgagctcaccacaaagggacgggtgccctaccctggga 1405
          ||||  ||  ||||||||||||||  ||   |   |||  |  ||  ||   |  ||  |||||  ||||
Db   1322 ggtcttttgggatcctgctgacggaaattgtcacccacggccgcatcccttacccaggga 1381

Qy   1406 tggtgaaccgcgaggtgctggaccaggtggagcggggctaccggatgccctgcccgccgg 1465
          ||   ||||  ||||||  |   |  |  |||||||  ||||||||  |||    ||||
Db   1382 tgaccaacccggaggtgattcagaacctggagcgaggctaccgcatggtgcgccctgaca 1441

Qy   1466 agtgtcccgagtccctgcacgacctcatgtgccagtgctggcggaaggagcctgaggagc 1525
          | |||||  |||   |||  || |  ||||||  | |  |||||||   |  ||   ||  |||||  |
Db   1442 actgtccagaggagctgtaccaactcatgaggctgtgctggaaggagcgcccagaggacc 1501

Qy   1526 ggcccaccttcgagtacctgcaggccttcctggaggactacttcacgtccaccgagcccc 1585
          ||||||||||  ||  |||||||      |  ||||||||||  |||||||  ||||  |||   ||
Db   1502 ggcccacctttgactacctgcgcagtgtgctggaggacttcttcacggccacagagggcc 1561

Qy   1586 agtaccagcc 1595
          ||||||||||
Db   1562 agtaccagcc 1571


RESULT  13
AAT71262
ID   AAT71262 standard; DNA; 1804 BP.
XX
AC   AAT71262;
XX
DT   30-MAR-1998  (first entry)
XX
DE   Human c-yes-2 gene.
XX
KW   Cognate transgene; human; c-yes-2; lymphoma; cellular immunogen; cancer;
KW   self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
KW   colon carcinoma; immunotherapy; proto-oncogene; ss.
XX
OS   Homo sapiens.
XX
```

SQ Sequence 4517 BP; 1437 A; 784 C; 955 G; 1341 T; 0 other;

Query Match 44.1%; Score 710.2; DB 22; Length 4517;
Best Local Similarity 70.1%; Pred. No. 6.9e-125;
Matches 955; Conservative 0; Mismatches 408; Indels 0; Gaps 0;

```
Qy    248 ccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggagacagacc 307
          | ||||| || || |  |||||||||  | |||||  |||||  ||||  ||       |||||
Db    476 caggtggtgttactatatttgtggccttatatgattatgaagctagaactacagaagacc 535

Qy    308 tgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagactggtggc 367
          | || || |||||  || ||   |  | || ||  | |||||  |||||  |||||  ||||||
Db    536 tttcatttaagaagggtgaaagatttcaaataattaacaatacggaaggagattggtggg 595

Qy    368 tggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtggcgccct 427
            ||    ||  ||   ||||||  |||  || || |||||  |||||  || ||  |||||
Db    596 aagcaagatcaatcgctacaggaaagaatggttatatcccgagcaattatgtagcgcctg 655

Qy    428 ccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggagtcagagc 487
          | || |||||  |||||  || || ||||||||||||||  ||    |||   ||  | ||
Db    656 cagattccattcaggcagaagaatggtattttggcaaaatggggagaaaagatgctgaaa 715

Qy    488 ggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagtgagacca 547
          | |||||  | |||  | |  || |   |||| |  ||| | ||  |||| |||||  || |
Db    716 gattacttttgaatcctggaaatcaacgaggtattttcttagtaagagagagtgaaacaa 775

Qy    548 cgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaacgtga 607
          | ||||||||  || | |||  ||   |  |||  |  ||  |    | |||   ||| ||||
Db    776 ctaaaggtgcttattccctttctattcgtgattgggatgagataaggggtgacaatgtga 835

Qy    608 agcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgcacccagt 667
          | ||||||||  ||  | ||  ||  ||||  ||  ||  | |||  |||||  ||  |  | ||  |
Db    836 aacactacaaaattaggaaacttgacaatggtggatactatatcacaaccagagcacaat 895

Qy    668 tcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctgtgccacc 727
          |  | |  ||||||  |  |||||    |||||  |  ||||  ||  ||||||  | ||||||
Db    896 ttgatactctgcagaaattggtgaaacactacacagaacatgctgatggtttatgccaca 955

Qy    728 gcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaaggatgcct 787
             | ||  ||  |||||  ||  ||     ||  ||  ||||||||  ||  ||  ||  ||||||  |
Db    956 agttgacaactgtgtgtccaactgtgaaacctcagactcaaggtctagcaaaagatgctt 1015

Qy    788 gggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgctttggcg 847
          ||||  ||||||||  ||  ||  ||||  ||  |||||  ||  ||  ||  ||  ||  ||  ||||
Db   1016 gggaaatccctcgagaatctttgcgactagaggttaaactaggacaaggatgtttcggcg 1075

Qy    848 aggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaagcctg 907
          | ||||||||||  ||  |||||  ||  |||||  |  ||  ||  ||||||||  ||  ||  ||  |
Db   1076 aagtgtggatgggaacatggaatggaaccacgaaagtagcaatcaaaacactaaaaccag 1135

Qy    908 gcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcatg 967
          |  ||  |||   |||||  ||  |||||  ||  ||  ||  |||  |  |||||  ||   |  ||  ||||
Db   1136 gtacaatgatgccagaagctttccttcaagaagctcagataatgaaaaaattaagacatg 1195

Qy    968 agaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtcacggagt 1027
          |  ||  ||  ||  |   |  ||||||||  |||||  ||  ||  ||  ||||||||  |||||  ||  |
Db   1196 ataaacttgttccactatatgctgttgtttctgaagaaccaatttacattgtcactgaat 1255

Qy   1028 acatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtacctgcggc 1087
            |||   ||  ||  ||  ||  |  ||  ||  ||  ||||  |     ||  |||||  ||  ||
Db   1256 ttatgtcaaaaggaagcttattagatttccttaaggaaggagatggaaagtatttgaagc 1315

Qy   1088 tgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggagcgga 1147
          |  ||  ||||||||  ||  ||||||||||||||  ||    ||  |||||  ||  |  ||  |  |
Db   1316 ttccacagctggttgatatggctgctcagattgctgatggtatggcatatattgaaagaa 1375

Qy   1148 tgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaagaacctggtgt 1207
          |||||||  |  |||||  ||  |||||  ||  ||  ||  ||  ||  ||  |||||  ||  ||  ||||
Db   1376 tgaactatattcaccgagatcttcgggctgctaatattcttgtaggagaaaatcttgtgt 1435

Qy   1208 gcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacggcgcggc 1267
          |||||  |  ||  ||||||||  |  ||  ||  |  ||||||||||||||  |||||  ||  |  |
Db   1436 gcaaaatagcagactttggtttagcaaggttaattgaagacaatgaatacacagcaagac 1495

Qy   1268 aaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggccgcttca 1327
          |||||||  |||||  ||  |||||  |||||  |||||  ||||||||  ||  |||||  ||  ||  |
Db   1496 aaggtgcaaaatttccaatcaaatggacagctcctgaagctgcactgtatggtcggttta 1555

Qy   1328 ccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccacaaagggac 1387
          |  ||  |||||  ||  ||  |||||  ||  ||  ||  ||||  ||  ||  ||    ||||||||  |
Db   1556 caataaagtctgatgtctggtcatttggaattctgcaaacagaactagtaacaaagggcc 1615

Qy   1388 gggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcggggctacc 1447
          |  |||||  ||  ||  ||  ||||||||||||  ||  ||  ||  ||  ||  ||||||||  ||  |||
Db   1616 gagtgccatatccaggtatggtgaaccgtgaagtactagaacaagtggagcgaggataca 1675

Qy   1448 ggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccagtgctggc 1507
          |||||||  |||||  |  ||  |||||  ||  |||||  ||  ||  |  |||  |  |||  |||
Db   1676 ggatgccgtgccctcagggctgtccagaatccctccatgaattgatgaatctgtgttgga 1735

Qy   1508 ggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggaggactact 1567
            ||||||  |||||  ||  |  ||  ||  ||  ||  ||  |  |||  |||||  ||||  ||||||||
Db   1736 agaaggaccctgatgaaagaccaacatttgaatatattcagtccttcttggaagactact 1795

Qy   1568 tcacgtccaccgagccccagtaccagcccggggagaacctcta 1610
          ||||  |  ||  |||||  ||||||||||  ||  ||  ||  |  ||
Db   1796 tcactgctacagagccacagtaccagccaggagaaaatttata 1838
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RESULT 11
AAS74489
ID AAS74489 standard; cDNA; 4517 BP.
XX
AC AAS74489;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #10293.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG10302.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 10293; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or

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Qy    700 tccaaacacgccgatggcctgtgccaccgcctcaccaccgtgtgccccacgtccaagccg 759
Db    747 atggaggtgaatgacgggctgtgcaacctgctcatcgcgccctgcaccatcatgaagccg 806

Qy    760 cagactcagggcctggccaaggatgcctgggagatccctcgggagtcgctgcggctggag 819
Db    807 cagacgctgggcctggccaaggacgcctgggagatcagccgcagctccatcacgctggag 866

Qy    820 gtcaagctgggccagggctgctttggcgaggtgtggatggggacctggaacggtaccacc 879
Db    867 cgccggctgggcaccggctgcttcggggatgtgtggctgggcacgtggaacggcagcact 926

Qy    880 agggtggccatcaaaaccctgaagcctggcacgatgtctccagaggccttcctgcaggag 939
Db    927 aaggtggcggtgaagacgctgaagccgggcaccatgtccccgaaggccttcctggaggag 986

Qy    940 gcccaggtcatgaagaagctgaggcatgagaagctggtgcagttgtatgctgtggtttca 999
Db    987 gcgcaggtcatgaagctgctgcggcacgacaagctggtgcagctgtacgccgtggtgtcg 1046

Qy   1000 gaggagcccatttacatcgtcacggagtacatgagcaaggggagtttgctggacttttctc 1059
Db   1047 gaggagcccatctacatcgtgaccgagttcatgtgtcacggcagcttgctggatttttctc 1106

Qy   1060 aaggggagacaggcaagtacctgcggctgcctcagctggtggacatggctgctcagatc 1119
Db   1107 aagaacccagagggccaggatttgaggctgccccaattggtggacatggcagcccaggta 1166

Qy   1120 gcctcaggcatggcgtacgtggagcggatgaactacgtccaccgggaccttcgtgcagcc 1179
Db   1167 gctgagggcatggcctacatggaacgcatgaactacattcaccgcgacctgagggcagcc 1226

Qy   1180 aacatcctggtgggagagaacctggtgtgcaaagtggccgactttgggctggctcggctc 1239
Db   1227 aacatcctggttggggagcggctggcgtgcaagatcgcagactttggcttggcgcgtctc 1286

Qy   1240 attgaagacaatgagtacacggcgcggcaaggtgccaaattccccatcaagtggacggct 1299
Db   1287 atcaaggacgatgagtacaacccctgccaaggttccaagttccccatcaagtggacagcc 1346

Qy   1300 ccagaagctgccctctatggccgcttcaccatcaagtcggacgtgtggtccttcgggatc 1359
Db   1347 ccagaagctgccctctttggcagattcaccatcaagtcagacgtgtggtcctttgggatc 1406

Qy   1360 ctgctgactgagctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcgag 1419
Db   1407 ctgctcactgagctcatcaccaagggccgaatcccctacccaggcatgaataaacgggaa 1466

Qy   1420 gtgctggaccaggtggagcggggctaccggatgccctgcccgccggagtgtcccgagtcc 1479
Db   1467 gtgttggaacaggtggagcagggctaccacatgccgtgccctccaggctgcccagcatcc 1526

Qy   1480 ctgcacgacctcatgtgccagtgctggcggaaggagcctgaggagcggcccaccttcgag 1539
Db   1527 ctgtacgaggccatggaacagacctggcgtctggacccggaggagaggcctaccttcgag 1586

Qy   1540 tacctgcaggccttcctggaggactacttcacgtccaccgagccccagtaccagcccggg 1599
Db   1587 tacctgcagtccttcctggaggactacttcacctccgctgaaccacagtaccagcccggg 1646

Qy   1600 gagaacctctag 1611
Db   1647 gatcagacatag 1658
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RESULT 9
AAX90200
ID AAX90200 standard; cDNA; 4517 BP.
XX
AC AAX90200;
XX
DT 23-SEP-1999 (first entry)
XX
DE Human yes1 encoding cDNA.
XX
KW Human; yes1; diagnosis; neuropsychiatric disorder; BAD; schizophrenia;
KW bipolar affective disorder; attention deficit disorder;
KW schizoaffective disorder; unipolar affective disorder;
KW Huntington's disease; Parkinson's disease; manic-depression; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 208..1839
FT /*tag= a
XX
PN WO9935290-A1.
XX
PD 15-JUL-1999.
XX
PF 07-JAN-1999; 99WO-US00297.
XX
PR 08-JAN-1998; 98US-0003944.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Chen H, Freimer NB;
XX
DR WPI; 1999-444203/37.
DR P-PSDB; AAY24421.
XX
PT Detection of a genetic mutation in the yes1 gene, useful for
PT diagnosis of a yes1 mediated neuropsychiatric disorder in a human
XX
PS Disclosure; Fig 1; 110pp; English.
XX
CC The present invention describes a method for detecting a genetic
CC mutation in the yes1 gene for the diagnosis of a yes1 mediated
CC neuropsychiatric disorder in a human. The method comprises detecting the
CC presence or absence of a genetic mutation in the yes1 gene of the
CC subject, where the genetic mutation is a substitution, insertion or a
CC deletion and results in the production of a yes1 protein having an amino
CC acid sequence other than the wild-type yes1 amino acid sequence and the
CC presence of the genetic mutation identifies a subject that has or is at
CC risk for developing a yes1 mediated neuropsychiatric disorder. Compounds
CC that bind to the yes1 protein, alter the amount of the protein, or alter
CC the activity of the yes1 gene product, are useful for treating a yes1
CC mediated neuropsychiatric disorder. The disorders include Huntington's
CC disease, Parkinson's disease, and especially bipolar-affected disorder
CC (BAD) also known as bipolar mood disorder (BP) or manic-depressive
CC illness. The method distinguishes neuropsychiatric disorders from
CC neurological disorders, which enables more accurate evaluation and
CC prescription of medical treatment. The present sequence represents the
CC human yes1 cDNA sequence.
XX
SQ Sequence 4517 BP; 1431 A; 781 C; 952 G; 1340 T; 13 other;

Query Match 44.1%; Score 710.2; DB 20; Length 4517;
Best Local Similarity 70.1%; Pred. No. 6.9e-125;
Matches 955; Conservative 0; Mismatches 408; Indels 0; Gaps 0;

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Qy    248 ccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggagacagacc 307
Db    476 caggtggtgttactatatttgtggccttatatgattatgaagctagaactacagaagacc 535

Qy    308 tgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagactggtggc 367
Db    536 tttcatttaagaagggtgaaagatttcaaataattaacaatacggaaggagattggtggg 595

Qy    368 tggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtggcgccct 427
Db    596 aagcaagatcaatcgctacaggaaagaatggttatatcccgagcaattatgtagcgcctg 655

Qy    428 ccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggagtcagagc 487
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Qy    614 acaagatccgcaagctggacagcggcggcttctacatcacctcccgcacccagttcaaca 673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 acaagatccgcaagctggacagcggcggcttctacatcacctcccgcacccagttcaaca 120

Qy    674 gcctgcagcagctggtggcctactactccaaacacgccgatggcctgtgccaccgcctca 733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gcctgcagcagctggtggcctactactccaaacacgccgatggcctgtgccaccgcctca 180

Qy    734 ccaccgtgtgccccacgtccaagccgcagactcagggcctggccaaggatgcctgggaga 793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ccaccgtgtgccccacgtccaagccgcagactcagggcctggccaaggatgcctgggaga 240

Qy    794 tccctcgggagtcgctgcggctggaggtcaagctgggccagggctgctttggcgaggtgt 853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 tccctcgggagtcgctgcggctggaggtcaagctgggccagggctgctttggcgaggtgt 300

Qy    854 ggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaagcctggcacga 913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaagcctggcacga 360

Qy    914 tgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcatgagaagc 973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 tgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcatgagaagc 420

Qy    974 tggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtcacggagtacatga 1033
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 tggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtcacggagtacatga 480

Qy   1034 gcaaggggagtttgctggactttctcaaggggagacaggcaagtacctgcggctgcctc 1093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 gcaaggggagtttgctggactttctcaaggggagacaggcaagtacctgcggctgcctc 540

Qy   1094 agctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggagcggatgaact 1153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 agctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggagcggatgaact 600

Qy   1154 acgtccaccgggaccttcgtgcagccaacatcctggtgggagagaacctggtgtgcaaag 1213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 acgtccaccgggaccttcgtgcagccaacatcctggtgggagagaacctggtgtgcaaag 660

Qy   1214 tggccgactttgggctggctcggctcattgaagacaatgagtacacggcgcggcaaggtg 1273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 tggccgactttgggctggctcggctcattgaagacaatgagtacacggcgcggcaaggtg 720

Qy   1274 ccaaattccccatcaagtggacggctccagaagctgccctctatggccgcttcaccatca 1333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ccaaattccccatcaagtggacggctccagaagctgccctctatggccgcttcaccatca 780

Qy   1334 agtcggacgtgtggtccttcgggatcctgctgactgagctcaccacaaagggacgggtgc 1393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 agtcggacgtgtggtccttcgggatcctgctgactgagctcaccacaaagggacgggtgc 840

Qy   1394 cctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcggggctaccggatgc 1453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 cctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcggggctaccggatgc 900

Qy   1454 cctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccagtgctggcggaagg 1513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 cctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccagtgctggcggaagg 960

Qy   1514 agcctgaggagcggcccaccttcgagtacctgcaggccttcctggaggactacttcacgt 1573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 agcctgaggagcggcccaccttcgagtacctgcaggccttcctggaggactacttcacgt 1020

Qy   1574 ccaccgagccccagtaccagcccggggagaacctctag 1611
          ||||||||||||||||||||||||||||||||||||
Db   1021 ccaccgagccccagtaccagcccggggagaacctctag 1058
```

RESULT 7
AAH18556
ID AAH18556 standard; cDNA; 3299 BP.
XX
AC AAH18556;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:18723.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 18723; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 3299 BP; 604 A; 981 C; 996 G; 718 T; 0 other;

Query Match 56.4%; Score 908; DB 22; Length 3299;
Best Local Similarity 98.9%; Pred. No. 3.8e-162;
Matches 914; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy    688 gtggcctactactccaaacacgccgatggcctgtgccaccgcctcaccaccgtgtgcccc 747
          | ||| | |       ||||||||||||||||||||||||||||||||||||||||||||||
Db    334 ggggcttgcgtgctggaacacgccgatggcctgtgccaccgcctcaccaccgtgtgcccc 393

Qy    748 acgtccaagccgcagactcagggcctggccaaggatgcctgggagatccctcgggagtcg 807
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 acgtccaagccgcagactcagggcctggccaaggatgcctgggagatccctcgggagtcg 453
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Db    823 tgccaccgcctgaccaacgtctgccccacgtccaagccccagacccagggactcgccaag 882

Qy    781 gatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgc 840
          || || ||||| ||||| ||||||||||||||||||||||||| |||||||| |||||||||
Db    883 gacgcgtgggaaatcccccgggagtcgctgcggctggaggtgaagctggggcagggctgc 942

Qy    841 tttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctg 900
          ||||| ||||| |||||||||||||||||||| |||||||| |||||||| || || |||
Db    943 tttggagaggtctggatggggacctggaacggcaccaccagagtggccataaagactctg 1002

Qy    901 aagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctg 960
          ||||| ||||| ||||| || ||||||||||||||||| ||||| || ||||||||||||
Db   1003 aagcccggcaccatgtccccggaggccttcctgcaggaagcccaagtgatgaagaagctc 1062

Qy    961 aggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtc 1020
          ||||||||||||||||| ||| |||| || ||||| || || |||||||| |||||||||
Db   1063 cggcatgagaagctggttcagctgtacgcagtggtgtcggaagagcccatctacatcgtc 1122

Qy   1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtac 1080
          || |||||||||||||||||| | ||||| || || ||||| |||| |||||||||
Db   1123 actgagtacatgagcaaggggagcctcctggatttcctgaagggagagatgggcaagtac 1182

Qy   1081 ctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtg 1140
          |||||||||| ||||| || || ||||||||||||| || || |||||||| || |||
Db   1183 ctgcggctgccacagctcgtcgatatggctgctcagattgcatccggcatggcctatgtg 1242

Qy   1141 gagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaac 1200
          ||| |||||||||||| ||||| ||||| || || |||||||||||||||| ||||||
Db   1243 gagaggatgaactacgtgcaccgagacctgcgggcggccaacatcctggtgggggagaac 1302

Qy   1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260
          |||||||||| ||||| |||||||||||||||| || |||||| || ||||| ||||||||
Db   1303 ctggtgtgcaaggtggctgactttgggctggcacgcctcatcgaggacaacgagtacaca 1362

Qy   1261 gcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggc 1320
          || |||||||||||||| |||||||||||||||||| || || || || ||||||||||||
Db   1363 gcacggcaaggtgccaagttccccatcaagtggacagcccccgaggcagccctctatggc 1422

Qy   1321 cgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccaca 1380
          || |||||||||||||||| || |||||||||| |||||||||||||||||| |||||
Db   1423 cggttcaccatcaagtcggatgtctggtccttcggcatcctgctgactgagctgaccacc 1482

Qy   1381 aagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcgg 1440
          ||||| |||||||| ||||| |||||||| ||| | ||||||||||||||||||||| ||
Db   1483 aagggccgggtgccatacccagggatggtcaacagggaggtgctggaccaggtggagagg 1542

Qy   1441 ggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccag 1500
          |||||||| |||||||||||||| ||||| |||||||| ||||| ||||||||||||||||
Db   1543 ggctaccgcatgccctgcccgcccgagtgccccgagtcgctgcatgacctcatgtgccag 1602

Qy   1501 tgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggag 1560
          |||||||||| ||| |||||||||||||||| || ||||||||||||||||||||||||
Db   1603 tgctggcggagggaccctgaggagcggcccacttttgagtacctgcaggccttcctggag 1662

Qy   1561 gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag 1611
          |||||||||| || ||||||||||||||| || |||||||| |||
Db   1663 gactacttcacctcgacagagccccagtaccagcctggagagaacctatag 1713
```

RESULT 5
AAQ46687
ID AAQ46687 standard; cDNA to mRNA; 1602 BP.
XX
AC AAQ46687;
XX
DT 23-DEC-1993 (first entry)
XX
DE Chicken pp60 c-src gene.
XX
KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX
OS Gallus gallus.
XX

PN WO9314193-A.
XX
PD 22-JUL-1993.
XX
PF 05-JAN-1993; 93WO-US000445.
XX
PR 06-JAN-1992; 92US-0820011.
XX
PA (UYYA) UNIV YALE.
XX
PI Bell L, Luthringer DJ, Madri JA, Warren SL;
XX
DR WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX
PT Genetically engineered endothelial cells - which exhibit enhanced
PT cell migration, urokinase-type plasminogen activator activity,
PT and reduced mononuclear cell adhesion and fibronectin prodn
XX
PS Disclosure; Page 59-62; 91pp; English.
XX
CC The DNA encoding a portion or (more preferably) the entire pp60
CC c-src polypeptide is used to transform endothelial cells.
CC Transformed cells produce increased amounts of pp60 c-src and have
CC improved therapeutic properties. They migrate at faster rates than
CC non-transformed counterparts; have an enhanced ability to inhibit
CC the formation of thrombi and/or dissolve thrombi once they have
CC formed and exhibit reduced mononuclear cell adhesion. They can also
CC be used to improve the success of surgical procedures such as
CC coronary angioplasty, heart bypass surgery, vessel graft and stent
CC implantation.
XX
SQ Sequence 1602 BP; 350 A; 503 C; 481 G; 268 T; 0 other;

Query Match 75.5%; Score 1216.6; DB 14; Length 1602;
Best Local Similarity 85.2%; Pred. No. 2.7e-220;
Matches 1373; Conservative 0; Mismatches 229; Indels 9; Gaps 1;

```
Qy      1 atgggtagcaacaagagcaagcccaaggatgccagccagcggcgccgcagcctggagccc 60
          ||||| |||| |||||||||||||||||  |||||||||| || ||||||||||||||
Db      1 atggggagcagcaagagcaagcccaaggaccccagccagcgccggcgcagcctggagcca 60

Qy     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120
          |||| | |   |||  |         || |  ||||| ||||||||||||||| ||||
Db     61 cccgacagcacccaccac---------gggggattcccagcctcgcagacccccaacaag 111

Qy    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgccccgcggccgccgag 180
          ||||  |  |||||   ||||||  |||||||    |||| |   ||| |||| |||||
Db    112 acagcagcccccgacacgcaccgcacccccagccgctcctttgggaccgtggccaccgag 171

Qy    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240
          |||||||| ||||| ||||||||| | || |||||||| || || |||||| | || ||
Db    172 cccaagctcttcgggggcttcaacacttctgacaccgttacgtcgccgcagcgtgccggg 231

Qy    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300
          | ||||| || || || ||||| || ||||| ||||| ||||| |||||  |||| ||
Db    232 gcactggctggcggcgtcaccactttcgtggctctctacgactacgagtcccggactgaa 291

Qy    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagac 360
          || ||| |||||||||||||||| || || || ||||||||||||||||||| || |||
Db    292 acggacttgtccttcaagaaaggagaacgcctgcagattgtcaacaacacggaaggtgac 351

Qy    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420
          |||||||||| || || ||||  |||||||||| |||||||||||| ||||| ||
Db    352 tggtggctggctcattccctcactacaggacagacgggctacatccccagtaactatgtc 411

Qy    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480
          |||||||| |||||||||||||||| |||||||| ||||| ||||||||  | ||||||
Db    412 gcgccctcagactccatccaggctgaagagtggtactttgggaagatcactcgtcgggag 471

Qy    481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540
          || |||||| | |||||||| | || |||||  | || |||||| | || || || ||
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RESULT   3
AAZ29700
ID   AAZ29700 standard; cDNA; 1759 BP.
XX
AC   AAZ29700;
XX
DT   22-MAR-2000  (first entry)
XX
DE   Wild-type chicken c-Src tyrosine kinase cDNA.
XX
KW   Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW   chicken; viral expression vector; replication competent; variant Src;
KW   inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
KW   diabetic retinopathy; osteoporosis; cancer; ss.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             112..1713
FT                   /*tag= a
FT                   /product= "Chicken c-Src tyrosine kinase"
FT                   /note= "Src used to modulate angiogenesis"
XX
PN   WO9961590-A1.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US11780.
XX
PR   29-MAY-1998;   98US-0087220.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Cheresh DA,  Eliceiri B,  Schwartzberg PL;
XX
DR   WPI; 2000-116335/10.
DR   P-PSDB; AAY44447.
XX
PT   Using tyrosine kinase Src for modulating angiogenesis in tissues useful
PT   in, e.g. treatment of chronic articular rheumatism -
XX
PS   Claim 1; Fig 1; 80pp; English.
XX
CC   The present sequence is the cDNA, encoding the wild-type chicken c-Src
CC   tyrosine kinase. This sequence encoding the Src protein, can be used to
CC   modulate angiogenesis. When the Src protein is inactivated, angiogenesis
CC   is inhibited, while when it is activated, angiogenesis is potentiated.
CC   The modified or variant Src can be used to treat inflammatory diseases
CC   like, arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis,
CC   osteoporosis and cancer associated disorders.
XX
SQ   Sequence 1759 BP; 370 A; 554 C; 533 G; 302 T; 0 other;

  Query Match             75.6%;  Score 1218.2;  DB 21;  Length 1759;
  Best Local Similarity   85.3%;  Pred. No. 1.4e-220;
  Matches 1374;  Conservative    0;  Mismatches  228;  Indels    9;  Gaps    1;

Qy      1 atgggtagcaacaagagcaagcccaaggatgccagccagcggcgccgcagcctggagccc 60
          ||||| |||| |||||||||||||||||  ||||||||||| || ||||||||||||||
Db    112 atggggagcagcaagagcaagcccaaggaccccagccagcgccggcgcagcctggagcca 171

Qy     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120
           |||| | |   |||  |         || |  ||||| ||||||||||||||| ||||
Db    172 cccgacagcacccaccac---------gggggattcccagcctcgcagacccccaacaag 222

Qy    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgcccccgcggccgccgag 180
           ||||  |  |||||   ||||||  ||||||||    |||| |   ||| |||| |||||
Db    223 acagcagccccgacacgcaccgcacccccagccgctcctttgggaccgtggccaccgag 282

Qy    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240
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                ||||||||  |||||  |||||||||  |  ||  ||||||||  ||  ||  ||||||  |  ||  ||
Db    283 cccaagctcttcgggggcttcaacacttctgacaccgttacgtcgccgcagcgtgccggg 342

Qy    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300
            |  |||||  ||  ||  ||||||  ||  |||||  |||||  |||||  |||||   ||||  ||
Db    343 gcactggctggcggcgtcaccactttcgtggctctctacgactacgagtcccggactgaa 402

Qy    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagac 360
          ||  |||  ||||||||||||||||  ||  ||  ||  ||||||||||||||||||||  ||  |||
Db    403 acggacttgtccttcaagaaaggagaacgcctgcagattgtcaacaacacggaaggtgac 462

Qy    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420
          ||||||||||||  ||  ||  ||||  ||||||||||||  ||||||||||||||  |||||  ||
Db    463 tggtggctggctcattccctcactacaggacagacgggctacatccccagtaactatgtc 522

Qy    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480
          ||||||||  ||||||||||||||||||  ||||||||  |||||  ||||||||   |  |||||||
Db    523 gcgccctcagactccatccaggctgaagagtggtactttgggaagatcactcgtcgggag 582

Qy    481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540
          ||  ||||||  |  ||||||||   |  ||  |||||   |  ||  ||||||  |  ||  ||  ||  ||
Db    583 tccgagcggctgctgctcaaccccgaaaaccccccggggaaccttcttggtccgggagagc 642

Qy    541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600
          |||||  ||  ||||||||||||  ||||||||  ||  ||||||||  ||||||||||||||||  |||
Db    643 gagacgacaaaaggtgcctattgcctctccgtttctgactttgacaacgccaaggggctc 702

Qy    601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db    703 aatgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcacgc 762

Qy    661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720
          ||  |||||||  ||||||||||||||||||||||||||||||||||||||||||  ||||||  ||
Db    763 acacagttcagcagcctgcagcagctggtggcctactactccaaacatgctgatggcttg 822

Qy    721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780
          ||||||||||  ||||  |||  ||||||||||||||||||  |||||  |||||  ||  ||||||
Db    823 tgccaccgcctgaccaacgtctgccccacgtccaagccccagacccagggactcgccaag 882

Qy    781 gatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgc 840
          ||  ||  |||||  |||||.||||||||||||||||||||||||  ||||||||  |||||||||
Db    883 gacgcgtgggaaatcccccgggagtcgctgcggctggaggtgaagctggggcagggctgc 942

Qy    841 tttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctg 900
          |||||  |||||  ||||||||||||||||||||||||  ||||||||  ||||||||  ||  |||
Db    943 tttggagaggtctggatggggacctggaacggcaccaccagagtggccataaagactctg 1002

Qy    901 aagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctg 960
          |||||  |||||  |||||  ||  ||||||||||||||||  |||||  ||  ||||||||||
Db   1003 aagcccggcaccatgtccccggaggccttcctgcaggaagcccaagtgatgaagaagctc 1062

Qy    961 aggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtc 1020
            ||||||||||||||||  |||  ||||  ||  |||||  ||  ||  ||||||||  |||||||||
Db   1063 cggcatgagaagctggttcagctgtacgcagtggtgtcggaagagcccatctacatcgtc 1122

Qy   1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggagacaggcaagtac 1080
          ||  ||||||||||||||||||||  |  |||||  ||  ||  |||||  ||||  |||||||||
Db   1123 actgagtacatgagcaaggggagcctcctggatttcctgaagggagagatgggcaagtac 1182

Qy   1081 ctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtg 1140
          ||||||||||  |||||  ||  ||  ||||||||||||||  ||  ||  ||||||||  ||  |||
Db   1183 ctgcggctgccacagctcgtcgatatggctgctcagattgcatccggcatggcctatgtg 1242

Qy   1141 gagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaac 1200
          |||  ||||||||||||||  |||||  |||||  ||  ||  ||||||||||||||||||  ||||||
Db   1243 gagaggatgaactacgtgcaccgagacctgcgggcggccaacatcctggtgggggagaac 1302

Qy   1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260
          ||||||||||  |||||  ||||||||||||||  ||  |||||  ||  |||||  ||||||||
Db   1303 ctggtgtgcaaggtggctgactttgggctggcacgcctcatcgaggacaacgagtacaca 1362

Qy   1261 gcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggc 1320
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```

```
XX
PS   Disclosure; Page 69-72; 91pp; English.
XX
CC   The DNA encoding a portion or (more preferably) the entire pp60
CC   c-src polypeptide is used to transform endothelial cells.
CC   Transformed cells produce increased amounts of pp60 c-src and have
CC   improved therapeutic properties. They migrate at faster rates than
CC   non-transformed counterparts; have an enhanced ability to inhibit
CC   the formation of thrombi and/or dissolve thrombi once they have
CC   formed and exhibit reduced mononuclear cell adhesion. They can also
CC   be used to improve the success of surgical procedures such as
CC   coronary angioplasty, heart bypass surgery, vessel graft and stent
CC   implantation.
XX
SQ   Sequence 1611 BP; 334 A; 507 C; 504 G; 266 T; 0 other;

  Query Match            99.9%;  Score 1609.4;  DB 14;  Length 1611;
  Best Local Similarity  99.9%;  Pred. No. 2.9e-294;
  Matches 1610;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 atgggtagcaacaagagcaagcccaaggatgccagccagcggcgccgcagcctggagccc 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 atgggtagcaacaagagcaagcccaaggatgccagccagcggcgccgcagcctggagccc 60

Qy     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gccgagaacgtgcacggcgctggcgggggcgctttccccgcctcgcagacccccagcaag 120

Qy    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgccccgcggccgccgag 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgccccgcggccgccgag 180

Qy    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc 240

Qy    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300

Qy    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacggagggagac 360
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    301 acagacctgtccttcaagaaaggcgagcggctccagattgtcaacaacacagagggagac 360

Qy    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccagcaactacgtg 420

Qy    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480

Qy    481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540

Qy    541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600

Qy    601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660

Qy    661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720

Qy    721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780

Qy    781 gatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 gatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgc 840

Qy    841 tttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctg 900
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Db    841 tttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctg 900

Qy    901 aagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 aagcctggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctg 960

Qy    961 aggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtc 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 aggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtc 1020

Qy   1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggggagacaggcaagtac 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 acggagtacatgagcaaggggagtttgctggactttctcaaggggggagacaggcaagtac 1080

Qy   1081 ctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtg 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ctgcggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtg 1140

Qy   1141 gagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaac 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 gagcggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaac 1200

Qy   1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ctggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacacg 1260

Qy   1261 gcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggc 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 gcgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatggc 1320

Qy   1321 cgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccaca 1380
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Db   1321 cgcttcaccatcaagtcggacgtgtggtccttcgggatcctgctgactgagctcaccaca 1380

Qy   1381 aagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcgg 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 aagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccaggtggagcgg 1440

Qy   1441 ggctaccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccag 1500
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Qy   1501 tgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 tgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggag 1560

Qy   1561 gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag 1611
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Db   1561 gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag 1611


RESULT  2
AAS87965
ID   AAS87965 standard; cDNA; 1699 BP.
XX
AC   AAS87965;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #23769.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
```

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 401 ACATCCCCAGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAG 450
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 131 yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 147

 451 TGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAA 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 148 TrpTyrPheGlyLysIleThrArgArgGluSerGluArgLeuLeuLeuAs 164

 501 TGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGA 550
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 164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThrL 181

 551 AAGGTGCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTC 600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 181 ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 197

 601 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 650
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 198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheTyrIl 214

 651 CACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACT 700
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 214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231

 701 CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG 750
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 231 erLysHisAlaAspGlyLeuCysHisArgLeuThrAsnValCysProThr 247

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 248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIleProAr 264

 801 GGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 850
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 264 gGluSerLeuArgLeuGluValLysLeuGlyGlnGlyCysPheGlyGluV 281

 851 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 900
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 281 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 297

 901 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCAT 950
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 298 LysProGlyThrMetSerProGluAlaPheLeuGlnGluAlaGlnValMe 314

 951 GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1000
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 314 tLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValValSerG 331

1001 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1050
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 331 luGluProIleTyrIleValThrGluTyrMetSerLysGlySerLeuLeu 347

1051 GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 1100
     ||||||||||||||||||  ||||||||||||||||||||||||||||||
 348 AspPheLeuLysGlyGluMetGlyLysTyrLeuArgLeuProGlnLeuVa 364

1101 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 1150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 364 lAspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValGluArgMetA 381

1151 ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 381 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGluAsn 397

1201 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAA 1250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 398 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAs 414

1251 TGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTC 1300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 414 nGluTyrThrAlaArgGlnGlyAlaLysProIleLysTrpThrAlaP 431

1301 CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 1350
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 431 roGluAlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSer 447

1351 TTCGGGATCCTGCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCC 1400
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 448 PheGlyIleLeuLeuThrGluLeuThrThrLysGlyArgValProTyrPr 464

1401 TGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGA 1450
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 464 oGlyMetValAsnArgGluValLeuAspGlnValGluArgGlyTyrArgM 481

1451 TGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAG 1500
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 481 etProCysProProGluCysProGluSerLeuHisAspLeuMetCysGln 497

1501 TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGC 1550
     |||||||||::::::||||||||||||||||||||||||||||||||||
 498 CysTrpArgArgAspProGluGluArgProThrPheGluTyrLeuGlnAl 514

1551 CTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGG 1600
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 514 aPheLeuGluAspTyrPheThrSerThrGluProGluTyrGlnProGlyG 531

1601 AGAACCTC 1608
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 531 luAsnLeu 533
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seq_name: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US93-00445-2

seq_documentation_block:

; Sequence 2, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820,011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 533 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; HYPOTHETICAL: No
; FRAGMENT TYPE: Complete Sequence

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 1385 GACGGGTGCCCTACCCTGGGATGGTGAACCGCGAGGTGCTGGACCAGGTG 1434
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  437 lyArgIleProTyrProGlyMetThrAsnProGluValIleGlnAsnLeu 453

 1435 GAGCGGGGCTACCGGATGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCA 1484
      ||||||||||||||||||       |||   :::||||||||||:::|||::
  454 GluArgGlyTyrArgMetValArgProAspAsnCysProGluGluLeuTy 470

 1485 CGACCTCATGTGCCAGTGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCT 1534
      ::::||||||      ||||||:::::::::||||||:::||||||||||
  470 rGlnLeuMetArgLeuCysTrpLysGluArgProGluAspArgProThrP 487

 1535 TCGAGTACCTGCAGGCCTTCCTGGAGGACTACTTCACGTCCACCGAGCCC 1584
      ||:::||||||::::::   |||||||||:::||||||:::||||||
  487 heAspTyrLeuArgSerValLeuGluAspPhePheThrAlaThrGluGly 503

 1585 CAGTACCAGCCC 1596
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  504 GlnTyrGlnPro 507
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seq name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:AAY29668

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s   documentation_block:
ID  AAY29668 standard; Protein; 496 AA.
XX
AC  AAY29668;
XX
DT  03-NOV-1999  (first entry)
XX
DE  Human src-family kinase laloo protein.
XX
KW  Human; laloo; src family kinase; SFK; proto-oncogene; gene therapy;
KW  developmental disorder; tumour formation; genetic vaccine.
XX
OS  Homo sapiens.
XX
PN  US5952213-A.
XX
PD  14-SEP-1999.
XX
PF  13-JAN-1998;  98US-0006675.
XX
PR  13-JAN-1998;  98US-0006675.
XX
PA  (UYRQ ) UNIV ROCKEFELLER.
XX
PI  Hemmati-Brivanlou A,  Weinstein DC;
XX
DR  WPI; 1999-527015/44.
    N-PSDB; AAZ08792.

PT  Isolated nucleic acids encoding vertebrate src-family kinases useful
PT  for the detection of proto-oncogenes and for diagnosing early
PT  developmental defects in embryos
XX
PS  Claim 22; Fig 1C; 42pp; English.
XX
CC  The present sequence represents a human src family kinase (SFK)
CC  designated laloo. Laloo plays a key role in the transformation of early
CC  stage embryonic cells to mesodermal cells and is likely to be a
CC  proto-oncogene. SFK nucleic acids may be used to produce SFK proteins
CC  and the functional domains of SFK, according to standard recombinant DNA
CC  methodologies. The laloo SFK protein is involved in the transformation
CC  of early stage embryonic cells into mesodermal cells and consequently
CC  mutations its nucleic acids are major causes of early developmental
CC  disorders. SFK is also thought to be a proto-oncogene involved in tumour
CC  formation. Therefore, the nucleic acids may be used to study the
CC  physiological and biochemical processes that cause early developmental
CC  defects and tumour growth. The nucleic acids may be used as probe to
CC  identify similar nucleic acids in biological samples and to quantify
CC  levels of expression. They may also be used to detect alterations within
CC  those nucleic acids which may be related to disease. They may also be
CC  used as primers in PCR to amplify and detect sequences encoding SFK.
CC  Additionally, the nucleic acids may be used in gene therapy protocols
CC  either as a genetic vaccine or as a transgene which is inserted into a
CC  patients genome to rectify inappropriate, or low levels of, SFK
CC  expression in the patient. The SFK proteins encoded by the nucleic acids
CC  may be used to assay for agents which modulate SFK expression and
CC  activity or as antigens in the production of antibodies against SFK. The
CC  proteins may also be administered to a patient to rectify inappropriate,
CC  or low levels of, SFK expression in a patient.
XX
SQ  Sequence   496 AA;


alignment_scores:
            Quality: 1441.00              Length:    538
              Ratio:  3.549                Gaps:     10
 Percent Similarity:  75.465   Percent Identity: 52.974

alignment_block:
 US-09-444-711-1 x AAY29668   ..

 Align seg 1/1  to: AAY29668  from: 1  to: 496

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     51 CCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGGGGCGCTTTCCCCG 100
        ||||   |||
     15 rLeuGlyPro..................................... 18

    101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCAC......CGC 144
                            |||   |||::::::   |||      :::
     19 ...................ProGluSerThrGlnThrHisTyrValLys 28

    145 GGCCCCAGCGCGGCCTTCGCCCCCGCGGCCGCCGAGCCCAAGCTGTTCGG 194
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     29 AspProThr..................................... 31

    195 AGGCTTCAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGC.... 240
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     32 .........SerThrValThrMetThrLysProGluArgSerSerLysH 45

    241 ..CCGCTGGCCGGTGGA......GTGACCACCTTTGTGGCCCTCTATGAC 282
          |||         |||         ::::::::::|||||||||||
     45 isProArgGluGluGlyGlnGluGluValValLeuLeuAlaLeuTyrAsp 61

    283 TATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAAAGGCGAGCGGCT 332
        |||:::::::            ||||||:::|||:::||||||:::::||
     62 TyrAspGlyValHisProGlyAspLeuThrPheArgLysGlyAspHisLe 78

    333 CCAGATTGTCAACAACACGGAGGGAGACTGGTGGCTGGCCCACTCGCTCA 382
        |   ::::::::::::   :::|||:::||||||   |||      :::|
     78 u...LeuLeuLysLysGluSerGlyGluTrpTrpGluAlaCysLeuIleS 94

    383 GCACAGGACAGACAGGCTACATCCCCAGCAACTACGTGGCGCCCTCCGAC 432
        ||||||||:::   |||::::::||||||||||||||||||      :::
     94 erThrGlyGluGluGlyPheValProSerAsnTyrValAlaTyrPheAsn 110

    433 TCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAGTC 482
        |||::::::::::|||||||||||||||      ::::::|||:::|||::
    111 SerLeuGluSerGluGluTrpTyrPheLysGlyMetSerArgLysGluAl 127

    483 AGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTTCCTCGTGC 532
        :||||||   |||||||::      |||      |||:::|||::::::|
    127 aGluArgGlnLeuLeuSerProValAsnLysSerGlyAlaPheMetIleA 144

    533 GAGAAAGTGAGACCACGAAAGGTGCCTACTGCCTCTCAGTGTCTGACTTC 582
        ||:::||||||||   ||||||::::::   |||||||||   |||
    144 rgAspSerGluThrMetLysGlyCysPheSerLeuSerValArgAsp... 159

    583 GACAACGCCAAGGGCCTCAACGTGAAGCACTACAAGATCCGCAAGCTGGA 632
              :::|||   :::||||||||||||||||||||||   |||||
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